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        Score
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Match
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.1530.854 Million cell updates/sec
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     NRPZ_MOUSE
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NRPI_MOUSE
NRPI_CHICK
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MEGM_ROUSE
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Pfam; PF00432; MAM; 1.
Pfam; PF00629; MAM; 1.
Pfam; PF000629; CUB; 2.
SMART; SM00042; CUB; 2.
SMART; SM00231; FAS8C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FAS8C_1; 2.
PROSITE; PS01285; FAS8C_1; 2.
PROSITE; PS01286; FAS8C_1; 2.
PROSITE; PS01286; FAS8C_2; 2.
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Result No.

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Q9y5y6 homo sa	054991 mus mus	Q16832 homo sapien	P98070 xenopus	Q62507 mus musc	057460 brachyda	P98063 mus musc	043405 homo sa	Q61398 mus mus	Q15113 homo sa	Q62371 mus mus	

### ALIGNMENTS

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H	precursor
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ທ :	Rattus norvegicus (Rat).
C)	Chordata;
n	a; Rodentia; Sciurognathi; Muridae;
× ×	NCBI_TaxID=10116;
ב סי	SEQUENCE FROM N.A.
ദേ	STRAIN-Sprague-Dawley;
⊳:	F C T V - T C C C C T
≥:	Ginty D.D.;
-	"Neuropilin is a semaphorin III receptor.";
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റ	NEURONAL POPULATIONS
ם נ	CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE
C) (	-1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
റ	CONTAINS 2 CUB DOMAINS.
n	CONTAINS 2
ח מ	SIMILARITY: CONTAINS 1 MAM DOMAIN.
G	This SWISS-PROT entry is copyright. It is produced through a collaboration
C	between the Swiss Institute of Bioinformatics and the EMBL outstation -
G	re are no res
റ	use by non-profit institutions as long as its content is in no way
3 C	modified and this statement is not removed. Usage by and for commercial
) C	entities requires a license agreement (See http://www.isb-sib.ch/announce/
3 C	or send an email to license@isb-sib.ch).
י ני	3,053330 1
<b>z</b> z	EMBL; ARUIG29/; AAC33338.1;
20 :	InterPro; IPR000859; CUB_domain.
70	IPR000421;
20	IPR000998; MAM_

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Matches
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EVLGCDWTDSKPTVETLGPTVKSEETTTPYPMDEDATECG
                                         DLITSDMADYQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG
                                                                                                                                                                                     FPRNPQAQPGEEW
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                                                                                      WEYIQDPRTQQPKLFEGNMHYDTPDIRRFEPVPAQYVRVYPERWSPAGIGMRL
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BY SIMI
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RESULT
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Pfam; PF00629; MAM; 1.
Pfam; PF00754; F5_F8_type_C; 2
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                EMBL; AF022856; AAC53379.1;
EMBL; AF022854; AAC53377.1;
EMBL; AF022855; AAC53378.1;
EMBL; AF022857; AAC53380.1;
EMBL; AF022858; AAC53381.1;
EMBL; AF022861; AAC53382.1;
                                                                SMART; SM
SMART; SM
PROSITE;
PROSITE;
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97470888; PubMed-9331348; Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.; "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not III.";
                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRP2_MOUSE STANDARD; PRT; 931 AA. 035375; 035373; 035374; 035376; 035377; 035378; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Neuropilin-2 precursor (Vascular endothelial cell
                                  Alternative
                                                                                                                                                                                                                                                                                     MGD; MGI:1100492;
                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an
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Mammalia; F
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InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM_domain.
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                                                     Fransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
SUBCELLULAR LOCATION: Type I membrane protection.
ALTERNATIVE PRODUCTS: 6 ISOFORMS; A22 (SHOWN HERE), A0, A5, A17,
B0 AND B5; ARE PRODUCED BY ALTERNATIVE SPLICING.
B0 AND B5; ARE PRODUCED BY ALTERNATIVE SPLICING.
B1 AND B5 ARE PRODUCED BY ALTERNATIVE SPLICING.
B1 AND B5 ARE PRODUCED BY ALTERNATIVE SPLICING. SOME NONEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,
INTESTINAL EPITHELIUM, KINNEY, LUNG AND SUBMANDITUALAR GLAND.
DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY. SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS. SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTESTINAL EPITHELIUM, KIDNEY, LUNG DEVELOPMENTAL STAGE: THE EXPRESSION IS DEVELOPMENTALLY REGULATED.
                                                                                                                                                                                                                                                                                                      P12259;
                                                                ; PS01180; CUB; 2.
; PS01285; FA58C_1;
; PS01286; FA58C_2;
; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                               equires a license agreement (S email to license@isb-sib.ch).
                                  splicing.
                                               Glycoprotein; Neurone;
                                                                                                                                                                                                                                                                                   Nrp2
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 POTENTIAL.
NEUROPILIN-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPLICING
                                                 Signal;
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                                               Repeat;
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; Murinae; Mus.
                                               Receptor
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|::|: ||||| |||:|| ||::|
TRFIRIRPQTWHIGIALRLELFGCRVTDAPCSNMIGMLSGLIADTQISASSTREYLWSPS
              SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT
                                                                                                                                                                          -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRY--
                                                                                                                                                                                                                                                                                               CGHLYTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY
                                                                                                                      IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR--
                                                                                                                                                           DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYL
                                                                                                                                                                                                EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPRMEIILQFLTFDLEHDPLQVGEG
                                                                                                                                                                                                                                     IEIRDGDSESADLLGKHCGNI-APPTIISSGSYLYIKFTSDYARQGAGFSLRYEIFKTGS
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931 AA;
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                                                                               WTPQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQ
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POLY-SER.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

MISSING (IN ISOFORM AA).

MISSING (IN ISOFORM AA).

MISSING (IN ISOFORM AB).

EDERNOIPETHGGEGYEDEIDDEYEGDWSNSSSTSGAGDP

SGGRESWLYTLDPLITTIAMSSLGVLLGATCAGLLLYCT

CSYSGLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA

-> GTLPPOTEPTUDTYPYQPIPAYRYYMAAGGAVLLAS
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CUB 1.
CUB 2.
P5/8 TYPE C 1.
P5/8 TYPE C 2.
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G -> I (IN
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GLSSRSGTTLENYFELYDGLKHKYKINHQKCCSEA -> G
GTLPGTEPTVDTVPVQFIPAKYYVNAGGAPLAVETTLE
ALVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                        VVLALVLHYHRERYAAKKTDHSITYKTSHYTNGAPLAVEPT LTIKLEQERGSHC (IN ISOFORM BO). VDIPETHGGEGYEDEIDDEYEGDWSNSSSTSGAGDPSSGK
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76F2443F411D2F63 CRC64;
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                                                                                                                                            RA Gluman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid
RT form of vascular endothelial growth factor (VESF) and of placenta
RT growth factor-2, but only neuropilin-2 functions as a receptor for
RT the 145-amino acid form of VEGF.";
LJ. Biol. Chem. 275:18040-18045(2000).

CC. -i- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC. AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC. -i- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
CC. SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
CC. -I- SUBURLALLAR LOCATION: Type I membrane protein.
CC. -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC. -I- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC. -I- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC. -I- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC. -I- SIMILARITY: CONTAINS 1 MAM DOMAIN.
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS AO AND A17).

MEDILINE-97470888; PubMed-9331348;

Chen H., Chedotal A., He Z.-G., Goodman C.S., Te

"Neuropilin-2, a novel member of the neuropilin
affinity receptor for the semaphorins Sema E and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Neuropilin-1 is expressed isoform-specific receptor 1 Cell 92:735-745(1998).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takashima S., Miao H.-Q., Neufeld G., Klagsbrun in-1 is expressed by endothelial and tumor cells pecific receptor for vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
; 014821;
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Primates;
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Catarrhini;
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i; Hominidae;
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PROSITE; PS01180;
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InterPro; IPR000421; FA58_C.
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es 142; Conservative
                                         ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
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                                                                                                                                                                    CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF
                                                                                                                                                                                   CGHLYTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY
 PQQSRLHGDDNGWTPNLDSN---
                PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF
                                  FSARYYLVHQEPLENFQ-----
                                                                   DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAK------
                                                                                  -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                   IEIRDGDSESADLLGKHCGNI-APPTIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGS
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PF00629; MAM; 1.
PF00754; F5_F8_t;
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SM00231; FA58C;
SM00137; MAM; 1.
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FA58C_2;
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InterPro; IPR000859; CUB_domain.
InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM_domain.
                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                   EMBL; D50086; BAA08789.1;
HSSP; P12259; 1CZT.
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MEDLINE-96353149; PubMed-8748368;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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SMART; SM00137; MAM; 1
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CSGMLGMVSGLISDSQITASNQADRNWMPENIRLVTSRTGWALP
                             KTSQSTSVSTKKEDETITRPIPSEETSTGINITTV-----AIPLVLLVVLVFAGMGIFA
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PS01286; FA58C_2;
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NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
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RESULT 5
NRP1_CHICK
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          InterPro; IPR00
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InterPro; IPR00
Pfam; PF00431;
Pfam; PF00629;
                                                                                                                      entities
or send a
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P79795;
                                                                               EMBL;
HSSP;
                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression of a cell adhesion molecule, neuropilin, developing chick nervous system.";
Dev. Biol. 170:207-222(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuropilin-1 precursor (A5 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujisawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takagi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-White leghorn; MEDLINE-95324761; Publ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC
(LAYERS D AND E OF SGFS), AMACRIN CELLS OF RETINA, N
DORSAL ROOT GANGLIA, ALSO EXPRESSED IN NONNEURONAL CE
BLOOD VESSELS IN THE ENTIRE EMBRYO.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERV SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
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P12259;
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                                                                                                                                   non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                  IPR000859; CUB_domain
IPR000421; FA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               te leghorn; TISSUE-Embryonic brain;
324761; PubMed-7601310;
Kasuya Y., Shimizu M., Matsuura T.
                                                                                                                        email
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license@isb-sib.cl
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IPR000998; 0431; CUB; 2

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RESULT 6
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PROSITE; PS01180; CUB; 2.

PROSITE; PS01285; FA58C_1;

PROSITE; PS01286; FA58C_2;
  16-0CT-2001
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PROSITE; PS50060; MAM_2; 1
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115; Conserv
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SM00137
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39, Created)
40, Last sequence update)
40, Last annotation updat
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67; Mismatches 180
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CUB 1.
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NEUROPILIN-1
                                      PRT;
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-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; MEMBRANE-BOUND (SHOWN HERE)
AND SOLUBLE/SNRP1; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND
SOLUBLE/SNRP1 ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-
BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT
TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PREDOMINANTLY IN THE
NERVOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN HEART
AND PLACENTA, MODERATELY IN LUNG, LIVER, SKELETAL MUSCLE, KIDNEY
AND PANCREAS; AND LOW IN ADULT BRAIN. THE SOLUBLE/SNRP1 ISOFORM IS
FOUND IN LIVER HEPATOCYTES, KIDNEY DISTAL AND PROXIMAL TUBULES.
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.; "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";
J. Biol. Chem. 275:18040-18045(2000).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gagnon M.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THE MEMBRANE-BOUND ISÓFORM IS A RECEPTOR INVOLVED IN DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIGENESIS, IN TORNATION OF CERTAIN NUERONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THE SOLUBLE/SNRP1 ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS, IT MAY ALSO INDUCE APOPTOSIS BY SEQUESTERING VEGF-165, MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRP1
                                                                                                                                                                                                                                                                                                                                                                    ISOFORM IS SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANGIOGENESIS.
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Primates;
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SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C;
SMART; SM00137; MAM; 1.
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TSEVTVRFESGSHISGRGFLLTYA---
                           LIQAPDPYQRIMINFNPHFDLEDRDCKYDYYEVFDGENENGHFRGKFCGKI-APPPYVSS
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                                                                                 RGL-----LALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEK
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IPR000421; FA58_C.
IPR001092; HLH_basic.
IPR000998; MAM_domain.
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                                                                                                    Conservative ·
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BY SIMILARITY.

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N-LINKED (GLCNAC. .) (POTENTIAL).

EFP -> GIK (IN SOLUBLE/SNRP1 ISOFORM).

MISSING (IN SOLUBLE/SNRP1 ISOFORM).

K -> E (IN REF. 1).

D -> H (IN REF. 2).

E -> D (IN REF. 2).
                                                                                                    76;
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CUB 1.
CUB 2.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                   Score 335; DB
Pred. No. 6.4e
76; Mismatches
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EXTRACELLULAR (
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PROBABLE.
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C -I- SUBCELLULAR LOCATION: Type I membrane protein.

C -I- SIMILARITY: BELONGS TO THE NEUBRYONIC NERVOUS SYSTEM.

C -I- SIMILARITY: CONTAINS 2 CUB DOMAINS.

C -I- SIMILARITY: CONTAINS 2 FS/8 TYPE C. DOMAINS.
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16-OCT-2001 (
Neuropilin-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Neuropilin is a semaphorin III receptor.";
Cell 90:753-762(1997).
-i- FUNCTION: RECEPTOR INVOLVED IN THE DEVE
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Mammalia; I
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(Rel. 40, Last annotation update)
1 precursor (Vascular endothelial)
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oa; Chordata;
ia; Rodentia;
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vengood D.V., Rowe E.G.,
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Sciurognathi; Muridae;
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PROSITE; PS01285; FA58C_1; 2
PROSITE; PS01286; FA58C_2; 2
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
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InterPro; IPR00998; MAM_domain.
Pfam; PF00431; CUB; 2.
Pfam; PF00629; MAM; 1.
Pfam; PF00754; F5_F8_type_C; 2.
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                                                                                                                                AGIIADELGGQISVLQRKGISRYEGILA-----NGVLSRDGSLSDKRFLFTSNG----CS
                                                                                                                                                                                                             GPFLFIKFVSDYETHGAGFSIRYEIFKRGPECSQNYTAPTGVIKSPGFPEKYPNSLECTY 175
                                                                                                                                                                                                                                       TSEVTVRFESGSHISGRGFLLTYA-----
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                        WLEIDLGEKKKITGIRTTG--STQSNENFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQ
                                                                             RSLSFEP ---
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                                                                                                                                                                                                                                                                                                                    RGLPLLCATLALALAGAFR-----SDKCGGTIKIENPGYLTSPGYPHSYHPSEKCEW 56
WIQVDLGLLRFVTAVGTQGAISKETKKKYYVKTYRVDISSNGEDWITLK--EGNKAIIFQ
                                                                                                      ---VGPHIGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVLQSSISEDFKCM
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illarity 24.1%;
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FA58C_2; 2.
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1; Mismatches 166
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Q28107; Q28108;

Q1-NOV-1997 (Rel. 35, Creater,

Q1-NOV-1997 (Rel. 35, Last sequence)

Q1-NOV-1997 (Rel. 40, Last annotation of the control of th
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Interpro; IPR000421; FA58_C.
Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00754; F5_F8_type_C; 2.
SMART; SM00231; FA58C; 2.
                                                                                                                                                             CHAIN
                                                                                                                                                                                     Repeat.
SIGNAL
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EMBL; M81441; AAA30513.1;
HSSP; P12259; ICZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guinto E.R., Esmon C.T., Mann K.G., Macgillivray R.T.;
"The complete cDNA sequence of bovine coagulation factor V.";
J. Biol. Chem. 267:2971-2978(1992).
-i- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
-i- SUBUNIT: Factor Va is composed of a heavy chain and a light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                  PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: Thrombin activates factor V proteolytically to the active cofactor, factor Va (formation of a heavy chain at the N-terminus and a light chain at the C-terminus).

PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY (BY SIMILARITY).

SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS. SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
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                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           license agreement
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F5/8 TYPE A 1.
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PLASTOCYANIN-LIKE
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Matches 88
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TISSUE-Brain;
MEDLINE-91337458; PI
Takagi S., Hirata T.
                                                                                                                                                                                                                                                                                                        NRPI_XENLA STANDARD; PRT; 928 AA.

P28824;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuropilin-1 precursor (A5 protein) (A5 antigen).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcamphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Yenopodinae; Xenopus.
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Neuron 7:255-307(1991).

Neuron 7:255-307(1991).

PUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOSENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORIAS (BY SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.

1- SUBCELLULAR LOCATION: Type I membrane protein.

1- SUBCELLULAR LOCATION: Type I membrane protein.

1- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER NEURONS.
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Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
"The A5 antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors.";
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PROSITE; PS01180;
PROSITE; PS01285;
PROSITE; PS01286;
PROSITE; PS50060;
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SMART; SM00137; MAM; 1.
PROSITE; PS00740; MAM_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00020; MAMDOM SMART; SM00042; CUB; 2.
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HSSP; P12259;
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1; PF00754; F5_F8_type_C; 7
                                                                                                                                                                                                                                           LLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKG- 77
EIVLEFESFELEADSN -- APGGQTCRYDWLG
                                                                                                      ESGSHISGRGFLLTY---
                                                                                                                                        QRIMINFNPHFDLEDRECKYDYVEVIDGDNANGQLLGKYCGKI-APSPLVSTGPSIFIRF
                                                                                                                                                                         KRLILRLG-DLDIESQTCASDYLLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRF
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                                                                    VSDYETPGAGFSIRYEVFKTGPECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFAPKMQ
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IPR000421; FA58_C.
IPR000998; MAM_domain.
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POTENTIAL.
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SULFATION.
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"Structure of the gene for human coagulation
Biochemistry 31:3777-3785(1992).
[2]
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Kane W.H., Davie E.W.;
"Cloning of a cDNA coding for human factor V, a blood factor homologous to factor VIII and ceruloplasmin.";
Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
                                                                                                                                                                                                                              MEDLINE-88107560; PubMed-2827731; Kane W.H., Ichinose A., Hagen F.S., "Cloning of CDNAs coding for the her region of human factor V, a blood cof internal repeats."; Biochemistry 26:6508-6514(1987).
MEDLINE=94264012;
Pittman D.D., Tomk
Kaufman R.J.;
                                                                                                 Shen N.L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
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Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W.,
Hewick R.M., Kaufman R.J., Mann K.G.;
"Complete cDNA and derived amino acid sequence of
"Complete cDNA and derived amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-92232668;
                                                                                                                                  PARTIAL SEQUENCE FROM N.A.
                                                                lymphocytes.
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           Tomkinson K.N.,
                       PubMed=8204629;
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S.-T., Pyati J.,
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            Michnick D.,
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                                                                       This SWISS-PROT entry is copyright. It is produced through a control between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                      Chan W.P., Lee C.K., Kwong Y.L., Lam C.K., Liang R.; "A novel mutation of Arg306 of factor V gene in Hong Blood 91:1135-1139(1998).
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"Mutation in blood coagulation
activated protein C.";
Nature 369:64-67(1994).
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MEDLINE-20052169; PubMed-10586886;
Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A.,
Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T.,
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IMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
IMILARITY: STRONG, TO COAGULATION FACTOR VIII.
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76:946-952(1990)
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de Ronde H.,
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ACTIVATION I
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tation; Thrombophilia; 3D-structure.
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                                                                                                                            AA TANDEM REPEATS
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RESULT
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HSSP; P12259; iCZT.
InterPro; IPR001117; Cu-oxidas
InterPro; IPR000421; FA58_C.
Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00754; F5_F8_type_C; 2.
SMART; SM00231; FA58C; 2.
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q9GLP1;
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16-OCT-2001
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Kim H.K.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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es 71; Conserv
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SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COM
2 PLASTOCYANIN-LIKE REPEARS.

SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
                                                                                                                                                                                                                                                                                    is calci
                                                                                                                                                                                                                                                                                               with factor Xa to activate prothrombin to thrombin. SUBUNIT: Factor Va is composed of a heavy chain and chain, noncovalently bound. The interaction between is calcium-dependent.
                                                                                                                                                                                                                                                            DOMAIN: Domain B contains 41 X 9 AA tandem repeats. and C2 may be involved in membrane binding.

PTM: Thrombin activates factor V proteolytically to
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precursor (Activated pro
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PLASTOCYANIN-LIKE 6
PS/8 TYPE C 1.
F5/8 TYPE C 2.
CLEAVAGE (BY THROME SIMILARITY).
CLEAVAGE (BY THROME SIMILARITY).
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HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (CONNECTING
(BY SIMILARITY).
PROBABLE.
          SIMILARITY)
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rPro; IPR000561; I
rPro; IPR000421; I
rPF00008; EGF; 1.
                                       HGNC:7036; MFGE8
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RX MEDILINE-9740585; PubMed-9260929;
RY MEDILINE-9740585; PubMed-9260929;
RT Taylor M.R., Couto J.R., Scallan C.D., Ceriani R.L., Peterson J.A.;
RT Taylor M.R., Couto J.R., Scallan C.D., Ceriani R.L., Peterson J.A.;
RT "Lactadherin (formerly BA46), a membrane-associated glycoprotein
RT expressed in human milk and breast carcinomas, promotes Arg-gly-Asp
RT (RGD)-dependent cell adhesion.";
RT DA Cell Biol. 16:861-869(1997).
CC -:- FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING. BINDS
CC -:- FUNCTION: MEDIN IS THE MAIN CONSTITUENT OF AORTIC MEDIAL AMYLOID.
CC -:- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
CC -:- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
CC -:- SUBCELLULAR LOCATION: MAMMARY EPITHELIAL CELL SURFACES AND AORTIC
CC --- STIMILAR LOCATION: ARGGED N-TERMINUS AITH MINOR SPECIES STARTING AT
CC --- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC --- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haeggqvist B., Naeslund J., Sletten K., Westermark G. Tjernberg L.O., Nordstedt C., Engstroem U., Westermar "Medin: an integral fragment of aortic smooth muscle lactadherin forms the most common human amyloid."; Proc. Natl. Acad. Sci. U.S.A. 96:8669-8674(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION. MEDLINE-97405885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and characterization of full abreast carcinoma protein BA46 from human J. Protein Chem. 17:143-148(1998).
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MEDLINE=98194924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99342076; PubMed-10411933
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Ceriani R.L.;
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MEDLINE-91371351; PubMed-1909932;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no restricted the state of the st
U58516; AAC50549.1;
S56151; AAB19771.1;
P08709; 1BF9.
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13908; PubMed=8639264;
Taylor M.R., Godwin S.G.
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Ol-NOV-1997 (Rel. 35, Created)
Ol-NOV-1997 (Rel. 35, Last sequence update)
Ol-NOV-1997 (Rel. 39, Last annotation update)
Lactadherin precursor (Milk fat globule-EGF fi
Ten Gn3 ganglioside synthase) (AGS) (MFGM)
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PROSITE; PS01022; E
PROSITE; PS01186; E
PROSITE; PS01285; E
PROSITE; PS01286; E
                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10116;
[1]
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                                                                                                            MEDLINE-96374422; PubMed-8780713; Ogura K., Wara K., Watanabe Y., Kohno "Cloning and expression of cDNA for Oganglioside."; Biochem. Biophys. Res. Commun. 225:932
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SIGNAL
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFGM_RAT
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Chem. Biophys. Res. Commun. 225:932-938(1996).
FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING. SEEMS PARTICIPATE IN THE O-ACCETYLATION OF GD3 GANGLICOSIDE SIALI SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: SPLEEN, LUNG, HEART, BRAIN AND MUSCLE SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVH---WSPGQARLQDQG--PSWASGD
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86; EGF_2;
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FA58C_2;
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E5/8 TYPE C 1.

F5/8 TYPE C 2.

F5/8 TYPE C 2.

CELL ATTACHMENT SITE
BY SIMILARITY.
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Pred. No. 6.5e-14;
3; Mismatches 55
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LACTADHERIN;
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                                                                                                                                               no K., Tai T.,
O-acetylation
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SMART; SM00181; EGF; 2.

SMART; SM00231; FA58C; 2.

PROSITE; PS00022; EGF_1; 2.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01186; FA58C_1; 2.

PROSITE; PS01186; FA58C_2; 2.
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InterPro; IPR001438; EGF_II.
InterPro; IPR000421; FA58_C.
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nilarity 26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 297.5;
Pred. No. 9.6e
4; Mismatches
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Hewick R.M.;
"Molecular clon
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21-JUL-1986
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Coagulation
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                                                                                                                                                                                                                                   Leyte A.,
Mertens K
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de Water N.S., Williams
Submitted (JUN-1997) to
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Toole J.J., Knopf J.L., Wozney J.M., SPIttman D.D., Kaufman R.J., Brown E.,
Amphlett G.W., Foster W.B., Coe M.L.,
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MEDLINE-92207952;
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Mammalia; Eutheria;
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312:342-347(1984)
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MEDLINE-89274393;
O'Brien D.P., Tudo
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Am. J. Hum.
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MEDLINE-90057680;
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"Membrane-binding pept
amphipathic structure
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MEDLINE-88220354;
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                                               ma M., Ware J., Yoshioka A., Fukui H., Fulche, arginine to cysteine amino acid substitution ombin cleavage site in a dysfunctional factor
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WZDLINE-90105723; PubMed-2104766;
MZDLINE-90105723; PubMed-2104766;
Arai M., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr
Phillips J.A. III, Janco R.L., Hoyer L.W.;
"Characterization of a thrombin cleavage site mutation
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"Cys) in the factor VIII gene of two unrelated patients
Cys) in the material-positive hemophilia A.";
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of the factor VIII gene",
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internal heavy chain thrombin cleavage site.";
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MEDLINE-90329422;
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Mancuso G., Morfini M., de Biasi R., Baudo F., Carbonara i
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Kazazian H.H.;
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Kazazian H.H., Antonarakis S.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT LEU-2326
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                     369
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                                                                                                                                                                              Local
                                                                                                                                                                                               Match
                                                                                                                        NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNH
                                                                                                      NSCSMPLGMESKAISDAQITASSYFTNMFAT----WSPSKARLHLQGRSNAWRPQVNN-
    FQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQ
                                                                         KPREWLEIDLGEKKKITGIRTTGSTOSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKV 368
                                                -PKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLF--FQNGKVKV
                                                                                                                                                                  62; Conser
                                                                                                                                                                                                                                                                                                 CYS-1728
                                                                                                                                                                                                                                                                                                                            6:65-71(1990)
                                                                                                                                                                                                                                                                 Higuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                AND CYS-1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND LEU-2326.
Pubmed-2105106;
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i M., Kazazian H.
A resulting from
                                                                                                                                                                                                                                                                                PubMed=2106480;
                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=2105906;
                                                                                                                                                                                                                                                                                                 AND ASP-1941
                                                                                                                                                                              7.6%;
37.6%;
                                                                                                                                                                                                                       lent gel electrophoresis
VIII gene.";
                                                                                                                                                                 32;
                                                                                                                                                              Score 285.5;
Pred. No. 8.2e
32; Mismatches
                                                                                                                                                                                                                                                                 Kasper
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 RESULT 15

REGULMOUSE

ID MARCH MOUSE

AC P21956

DT 01-AUG

DT 16-OCT

DE (Sperm

GN. MFGER.

OC MAMMAL

RT FOLONA

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                                                                                     PRINTS; PRO0010; EGFBLOOD.
SMART; SM00181; EGF; 2.
SMART; SM00231; EA58c; 2.
SMO0231; PA58c; 2.
PROSITE; PS01022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01286; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P21956; P97800;
01-AUG-1991 (Rel. 19,
01-AUG-1991 (Rel. 19,
16-OCT-2001 (Rel. 40,
                                             Signal;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                           EMBL; M38337;
EMBL; Y11684;
PIR; A36479; A
   DOMAIN
DOMAIN
                                                                                                                                                                                      Interpro; IPR000561; EGF-11ke
Interpro; IPR001438; EGF II.
Interpro; IPR000421; FA58_C.
Pfam; PF00008; EGF; 2.
Pfam; PF00754; P5_F8_Type_C;
                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensslin M.A.;
Submitted (NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stubbs J.D., Lekutis C., Singer K.I Srinivasan U., Parry G.; Srinivasan U., Parry G.; "cDNA cloning of a mouse mammary er reveals the existence of epidermal to factor VIII-like sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
Lactadherin precursor (Milk fat globule-EGF
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MEDLINE=91046008; Pul
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                MGI:102768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MAY
                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
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                                                                      Glycoprotein;
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: A36479.
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148
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CAA72380.1;
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tis C., Singer K.L.,
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AMMARY EPITHELIAL CEI
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ED IN PHOSPHOLIPID BINDING. Z
LACTADHERIN.
EGF-LIKE 1.
EGF-LIKE 2.
F5/8 TYPE C:
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Sciurognathi; Muridae
                                                                         EGF-like domain;
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SURFACES

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LACTATING

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EMBL

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Matches 112; Conserv
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CONFLICT
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                                                                                                                                    CTLRFELLGCELHGCLEPLGLKNNTIPDSQMSASSSYKTWNLRA--FGWYPHLGRLDNQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGLVCNETERGPCSPNPCYNDAKCLVT-LDTQRGDIFTEYICQCPVGYSGIHCETETNYY 114
                                                                                       WKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC 412
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463 AA;
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51465 MW;
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23.4%;
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CELL ATTACHMENT SITE (POTENTIAL).

BY SIMILARITY.

AN-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

S -> F (IN REF. 2).

ETNYYMLDGEYMETTAVPNTAVPTPAPTPDLSNNLASR ->

G (IN REF. 2).

ETNYYMLDGEYMETTAVPNTAVPTPAPTPDLSNNLASR ->

G (IN REF. 2).

T -> S (IN REF. 2).

L -> S (IN REF. 2).

ETNYCHCTORYCOTECTER STORYCOMMENT S
                                                                                                                                                                                                                                 -----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 276.5; DB 1; Length 463;
Pred. No. 3.4e-12;
9; Mismatches 118; Indels 189
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Maximum Match 100%
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Q9H2E3
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#### Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Kadota K., Matsuda H.A., Gojobori T., Bono H., Kasukawa T., Saito R., A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., A Kleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Ki Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., A Kuhal P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., A Kuhal L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A Gustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P., A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A Havashizaki Y., Storch K., Schoenbach C., Seya T., Shibata Y., Kawaji H., Kohtsuki S., SEQUENCE FROM N.A. STRAIN-C57BL/6J; TISSUE-TESTIS; MEDLINE-21085660; PubMed-11217851; Kawai J., Shinagawa A., Shibata K., Eukaryota; Metazoa; Mammalia; Eutheria; 01-JUN-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. NCBI\_TaxID=10090; Mus musculus (Mouse). 4631413K11Rik protein Q9D4J3; Q9D4J3 PRELIMINARY; Chordata; Rodentia; 17, 17, 21, Last sequence update) Last annotation update) Created) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus PRT; Yoshino M., Itoh M., 503 ₹

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Nature 409:685-690(2001).

1 CUB DOMAIN

Hayashizaki Y.: "Function of a full-length

mouse cDNA collection.";

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Mammalia; Eutheria; I
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InterPro; IPRO004043; LCCL_dom.
Pfam; PF00431; CUB; 1.
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Chordata; Rodentia;
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Pred. No. 6.9
Craniata; Vertebrata; Sciurognathi; Muridae;
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RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schiml L., Stubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninoi P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

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SMART; SM00042; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
SECULATION OF THE PROSITE PS0134 MW;
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Best Local
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ
EMBL; BC026771; AAH26771.1; -.
SEQUENCE 432 AA; 46798 MW; AD3FB42B24CD491
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 4631413K11 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8R327
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       AAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTIT
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VPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFE
|||||| || ||| ||::|||| |:
                                                                                                                                                                         GCSRSLSFEPDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREW
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                                                                                                                                   LEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNS
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                                                                                              NFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTSQSTSVS
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                  Score 1535; DB 11;
Pred. No. 6.9e-110;
6; Mismatches 72;
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Best Local S
Matches 275
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01-DEC-2001
01-DEC-2001
01-JUN-2002
Endothelial
                                                                                                                                                                                                                                                                                                                                                                    Kobuke K., Furukawa Y., Sugai M., Tanigaki K., Of Matsumori A., Sasayama S., Honjo T., Tashiro K.; "ESDN, a Novel Neuropilin-like Membrane Protein C Cells with the Longest Secretory Signal Sequence Up-regulated after Vascular Injury."; J. Biol. Chem. 276:34105-34114(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                            VTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIE-SQTCASDYL-LFT
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         VLQRKGISRYEGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQ
                                          LERASHYLKTEYSKFCPAGCRDVAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQIS
                                                                       GIGVSRTEIGKYCGLGLQMNQSIESKGSEVTVLFMSGTHAAGRGFLASYSVIDKEDLITC
                                                                                   S---SSDQYGPYCG-SMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYASSDHPDLITC
                                                                                                                 VLGPESGTLTSINYPHTYPNSTVCEWEIRVRTGERIRIKFGDFDIEDSDYCHLNYLKIFN
                                                                                                                                                        PQGPGGPAAPAATGRAALPSAGCCPLPPGRNSSSRPRLLLLLLLLLLQDAGGQQGDGCGHT
                                                                                                                                                                             LATESGHPDSQKPPTHPGTSDSYSAPRDCLTPLNQTAMTALL
                              LDTVSNFLEPEFSKYCPAGCLLPFAEISGTIPHGYRDSSPLCMAGIHAGVVSNVLGGQIS
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1 (TrEMBLrel. 19, Las
2 (TrEMBLrel. 21, Las
1 and smooth muscle c
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Last sequence update;
Last annotation update;
Le cell-derived neuropilin-like
                                                                                                                                                                                                 Score 1062; DB 11;
Pred. No. 4.9e-73;
1; Mismatches 274;
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Eukaryotes, Is
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            EMBL; AF387549; AAL30180.1; -. InterPro; IPR000859; CUB_domain. InterPro; IPR000421; FA58_C. InterPro; IPR004043; LCCL_dom. Pfam; PF00431; CUB; 1. Pfam; PF00754; F5_F8_type_C; 1. PROSITE; PS01180; CUB; 1.
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Q91ZV2;
01-DEC-2001
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Endothelial
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ESDN.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
   DNA-binding;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
and smooth muscle cell-derived neuropil
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Sciurognathi; Muridae;
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TGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVA
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. 19, Created)
. 19, Last sequence update)
. 21, Last annotation update)
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Pfam; PF00754; P5_F8_type_C; 1.
PROSTTE; PS01180; CUB; 1.
DNA-binding; Transcription regulation.
SEQUENCE 775 AA; 85034 MW; 3D06F81EF2337010 CRC64;
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MATSUMOTI A., SASAYAMA S., HONJO T., TAShiro K.;
"ESDN, a NOVEl Neuropilin-like Membrane Protein Cloned
Cells with the Longest Secretory Signal Sequence among
Up-regulated after Vascular Injury.";
U- BIOL Chem. 276:34105-34114(2001).
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InterPro; IPR000421; FA58_C.
InterPro; IPR004043; LCCL_dom.
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                          RKGSTFRPMDTDAEEAG-VSTDAGGHYDCPQRAGRHEYALPLAPPEPEYATPIV---ERH
                                                                                                                                                                                                          ----VAIPLVLLVVLVFAGMGIFAAF------RKKKKKGS---PYGSAEAQKTDCWKQ
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HQRSTFKP--EEGKEAGYADLDP---YNSPGQEVYHAYAEPLPITGPEYATPIIMDMSGH
                                                                                                                                                                              VTKDVALAAVLVPVLVMVLTTLILILVCAWHWRNRKKKTEGTYDLPYW~---DRAGWWKG
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                                                                                        MKQFLPAKAVDHEETPVRYSSSE--VNHLSPREVT---TVLQADSAEYAQPLVGGIVGTL
                                                                                                                                                                                                                                                                                                                     --GNDSLVWRKTSQSTSVSTKKEDETITRPI-----PSEET--STGINITT----
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ROShikawa K., Osada H., Kozaki K., Konishi H., Masuda Roshikawa K., Mitsudomi T., 'Nakao A., Takahashi T.;
Tatematsu Y., Mitsudomi T., 'Nakao A., Takahashi T.;
"Significant up-regulation of a novel gene, CLCPl, in metastatic lung cancer subline as well as in lung canconcogene 0:0-0(2002).
CMBL; AB073146; BAB91138.1; -.
EMBL; AB073146; BAB91138.1; -.
SEQUENCE 775 AA; 85073 MW; 6D07223B21BE5A42 CRC64
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NEDO human cDNA sequencing project.";

Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pred. No. 4.3e-57;
                                                    Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
                              Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                          Q8QZY7
Q8QZY7;
01-JUN-2002
01-JUN-2002
                                               SEQUENCE FROM N.A.
STRAIN-ILS, AND ISS;
MEDLINE-21363810; PubMed-11471062;
Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang
Beeson M., Gordon L., Bennett B., Johnson T.E., Sik
"High-throughput sequence identification of gene co
                                                                                                                                                                                                                                              Neuropilin-2(a.,
Nus musculus (Mouse).
Mus musculus (Motazoa; Chordata;
heria; Rodentia;
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SEQUENCE
Shibata T
     Mamm.
[2]
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                           Genome
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PRELIMINARY;

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Craniata; Vertebrata; Sciurognathi; Muridae;

Eutel Murinae;

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12:657-663(2001)

ang F., Sikela

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InterPro; IPRO04043; LCCL_dom.
Pfam; PF00431; CUB; 1
Pfam; PF00754; F5_F8_type_C; 1.
SMART; SM00042; CUB; 1.
PROSITE; PS01180; CUB; 1.
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EMBL; D29810; BAA18909.1; -.
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NON_TER 1
SEQUENCE 364 AA; 3
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InterPro; IPR000421; FA58_C.
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GNKRIITRMVRNNFLPPIIAR
                   GNSN-FRDPVQNNFIPPIVAR
                                                                                                               EIDLGEKKKITGIRTTGSTQ-SNFNFYVKS---FVMNFKNNNSKWKTYKGIVNNEEKVFQ
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                                                                             QIDLNKEKKITGIITTGSTMVSTITMCLPTESCTVMMGRNG
                                                                                                                                                        SGGD-RGSSNNSITVLEW--TDHTGQENSWKPKKSQAE---KTWTALGAFATDE--YQWL
                                                                                                                                                                                               PDGQIRASSS-------WQSVNESGDQVHWSPGQARLQDQGPSW-ASGDSSNNHKPREWL
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147; Conserv
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Pred. No. 8.1e-36;
1; Mismatches 124;
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Q9H2E4;
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EMBL; AF483507; AAL90781.1; -.
SEQUENCE 926 AA; 104054 MW; 8073D6478C9A8467 CRC64;
                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
    SEQUENCE
                   NCBI_TaxID-9606;
                                                                                               NRP2.
                                                                                                            Neuropilin-2b(0)
                                                                                                                                                                                                                                                                          577
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                                                                                                                                                                                                                                                                     RWSPAGIGMRLEVLGCDWTDSKPTVETLGPTVKSEETTTPYPMDEDATECG
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                                                                                                                                                                                                                                                                                                                                    KFKVSYSLNGKD
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                                                                                                                        Created)
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Pred. No. 1.
                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           PRT;
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Best Local S
Matches 142
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SMART; SM00231; FA58C; 2...
SMART; SM00231; FA58C; 2...
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01286; FA58C_1; U
PROSITE; PS01286; FA58C_2; 2
PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: 1
-!- SIMILARITY: CONTAINS 2
-!- SIMILARITY: BELONGS TO
-!- SIMILARITY: CONTAINS 1
EMBL; AF280544; AAG41403.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; CUB;
Pfam; PF00754; F5_F8
Pfam; PF00629; MAM;
PRINTS; PR00020; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rossignol M., Gagnon M.L., Klagsbrun M.; "Genomic Organization of Human Neuropilin-1 and Neu Identification and Distribution of Splice Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 70:211-222(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000421;
InterPro; IPR000998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 142; Conserv
                                                                                                                                                                                                                      VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA
: | | | : |:||: || || || ||
                                                                                                                                                                                                                                                                                                                       PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYYKSF
                                                                                                                                                                                                                                                                                                                                                                                              ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY
                                   CWKQIKYPFARHQSA-EFTISYD-----
                                                                        QAQPGEEWLQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVRKFKVSYSLNGKD:
                                                                                                                                                                         LKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP------IP
                                                                                                                                                                                                                                                                                                   PQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQGAISRETQNGYYVKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF
-WEYIQDPRTQQPKLFEGNMHYDTPDIRRFDPIPAQYVRVYPERWSPAGIGMRLEVLGCD
                                                                                                          SEETSTGINITTVAIPLVLLVVLVFAGMG----IFA----AFRKKKKKGSPYGSAEAQKTD
                                                                                                                                                                                                                                                                                                                                                                              FSARYYLVHQEPLENEQ-----CNVPLGMESGRIANEQISASSTY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAK------DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPKMEIILQFLIFDLEHDPLQVGEG
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                                                                                                                                                 LRLELFGCRVTDAPCSNMLGMLSGLIADSQISASSTQEYLWSPSAARLVSSRSGWFPRIP
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CONTAINS 2 CUB
BELONGS TO THE
CONTAINS 1 MAM
AAG41403.1;
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FA58_C.
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Pred. No. 3.6e-18;
9; Mismatches 255;
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B DOMAINS.
E NEUROPILIN 1
M DOMAIN.
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1F3107A9CC665EA2
                                   -----NEKEMTQKLDLITSD
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537 594

WTD-SKPTVKTLGPTVKSEETTTPYPTEEE----ATECG

575 627

MADYQQPLMIGTGTVTRKGSTFRPMDTDAEEAGVSTDAG

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RESULT 12
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Best Local
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SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00231; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; UPROSITE; PS01285; FA58C_2; 2
PROSITE; PS01286; FA58C_2; 2
PROSITE; PS01060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIINE-20564205; PubMed-11112349;
ROSSignol M., Gagnon M.L., Klagsbrun M.;
"Genomic Organization of Human Neuropilin-1 and Neu
"Genomic Organization of Human Neuropilin-1 and Neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00431; CUB; Pfam; PF00754; F5_F1 Pfam; PF00629; MAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
-I- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-I- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-I- SIMILARITY: CONTAINS 1 MAM DOMAIN.
EMBL; AF281074; AAG41899.1; -.
HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000859; CUB_domain.
InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
SEQUENCE 90
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Genomics 70:211-222(2000).
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                                                                                                                                                                                                                                                                                                                                                                LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS
                                                                                                                                                                                                                                                                                                                                                                                                                  CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF 87
                                                                                                                                                                                                             EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPKMEIILQFLIFDLEHDPLQVGEG
          FSARYYLVHQEPLENFQ-----
                                                         ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                           DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAK-----
                                                                                                                                                        -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                                                                                                                                                                                              IEIRDGDSESADLLGKHCGNI-APPTIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901 AA;
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ilarity 22.2%;
Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUB; 2.
FA58C_1; UNKNOWN_1.
FA58C_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _F8_type_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101381 MW;
                                                                                                                                                                                                                                            Receptor;
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16,
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Last sequence update)
Last annotation updat
-CNVPLGMESGRIANEQISASSTY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 351.5;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1310304AFD086AB CRC64;
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nts and Soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                     Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
Pfam; PF000734; F5_F8_type_C; 2
Pfam; PF000754; F5_F8_type_C; 2
Pfam; PF000629; MAMDOMAIN.
SMART; SM00042; CUB; 2.
SMART; SM00031; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; UNK
PROSITE; PS01285; FA58C_2; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS01286; MAM; 1.
Glycoprotein; Neurone; Recepto:
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Q9H2E3;
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 90
                                                                                                                                                                                      InterPro; IPR000859; CUB_domain.
InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM_domain.
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01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                             Rossignol M., Gagnon M.L., Klagsbrun M.;
"Genomic Organization of Human Neuropilin-1 and Neuropilin-2 Gidentification and Distribution of Splice Variants and Soluble
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=20564205;
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            Similarity
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                                             101955
           9.3%;
                                           Receptor;
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Last annotation update)
           Score 351.5; DB 4; Pred. No. 3.7e-18;
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           -1- SUBCELLULAR LOCATION: TYPE I
-1- SIMILARITY: CONTAINS 2 CUB D
-1- SIMILARITY: BELONGS TO THE N
-1- SIMILARITY: CONTAINS 1 MAM D
EMBL; AF281074; AAG41900.1; -.
HSSP; P12259; 1CZT.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                            SEQUENCE FROM N.A.

MEDLINE=20564205; PubMed=11112349;

Rossignol M., Gagnon M.L., Klagsbrun M.;

"Genomic Organization of Human Neuropilin-1 and Neuropilin-2 Ge
"Gentification and Distribution of Splice Variants and Soluble
                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                     Genomics 70:211-222(2000).
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                                                                                                                                                                                      NCBI_TaxID=9606;
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                                     NEUROPILIN DOMAIN.
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SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01286; FA58C_1; U
PROSITE; PS01286; FA58C_2; 2
           Q8UVRO;
Q8UVRO;
01-MAR-2002
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01-JUN-2002
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InterPro; IPR000999; MAM_dom.
Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C;
Pfam; PF00759; MAM; 1.
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PROSITE; PS01285; FA58C_1; UNKNOWN_1.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS50060; MAM_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY
                                                                                                                                        WTD-SKPTVETLGPTVKSEETTTPYPTEEE----ATECG
                                                                                                                                                                MADYQQPLMIGTGTVTRKGSTFRPMDTDAEEAGVSTDAG 575
                                                                                                                                                                                                                       CWKQIKYPFARHQSA-EFTISYD--------NEKEMTQKLDLITSD
                                                                                                                                                                                                                                                                                                                                                                                                                                  PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                                             -WEYIQDPRTQQPKLFEGNMHYDTPDIRRFDPIPAQYVRVYPERWSPAGIGMRLEVLGCD
                                                                                                                                                                                                                                                   QAQPGEEWLQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVRKFKVSYSLNGKD-----
                                                                                                                                                                                                                                                                              SEETSTGINITTVAIPLVLLVVLVFAGMG---IFA----AFRKKKKKGSPYGSAEAQKTD
                                                                                                                                                                                                                                                                                                       LRLELFGCRVTDAPCSNMLGMLSGLIADSQISASSTQEYLWSPSAARLVSSRSGWFPRIP
                                                                                                                                                                                                                                                                                                                                   LKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP----
                                                                                                                                                                                                                                                                                                                                                              KLEVSTNGEDWMYYRHGKNH--KVFQANNDATEVVLNKLHAPLLTRFVRIRPQTWHSGIA
                                                                                                                                                                                                                                                                                                                                                                                        VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA
                                                                                                                                                                                                                                                                                                                                                                                                                     PQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQGAISRETQNGYYVKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSARYYLVHQEPLENFQ-----CNVPLGMESGRIANEQISASSTY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPKMEIILQFLIFDLEHDPLQVGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEIRDGDSESADLLGKHCGNI-APPTIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------HPDLITC----LERASHYLKTEYSKF---------
             (TrEMBLrel.)
(TrEMBLrel.)
(TrEMBLrel.)
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                                                                    PRELIMINARY;
receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 351.5; DB 4; 22.2%; Pred. No. 3.7e-18; co. Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ne; Receptor;
101956 MW;
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           20,
             Last sequence update)
Last annotation update
                                        Created)
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EB183F265457B0B9
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             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Herrog Y., Kalcheim C., Kahane N., Reshef R., Neufeld G.;
"Differential expression of neuropilin-1 and neuropilin-2 in arteries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01285; FA58C_1; UNKNOWN_2.
PROSITE; PS01286; FA58C_2; UNKNOWN_2.
PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
               375 FRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQIT 415
                                                                                                                                     292
                                                                                                                                                                                                      244 VLSLTFHTDLAVAKDGFSAQYYLIQQEVPENFQCNVPLGMES--GRISNM------
                                                                                                                                                                                                                                                                                                                                            124
390 ATEVVLNKIHSPVLTRFVRIRPQSWHNGIALRLELYGCRIT
                                                                 332 DLHFLTVLTAIATQGAISRETQNGYYVRTYKLEVSTNGEDWMYRHGKNH--KTFQANED
                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                          167 KTE----YSKF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                          65 NQKIILNFNPHFEIEKHDCKYDFIEIRDGDSEAADLLGKHCGNI-APPTIISSGSSLYIK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                           77 GKRLILRLG-DLDIESQTCASDYLLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 GLLALLLAVSAPLRIQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           veins."
                                                                                                                                   -----QISASSTY-----SDGRWTPQQSRLNSDDNGWTPNVDSN----KEYLQV
                                                                                                                                                                   RSLSFEPDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEI 316
                                                                                                                                                                                                                        LCKAAIHA--GIIADELGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLFTSNGCS 256
                                                                                               DLGEKKKITGIRTTG--STQSNENFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSN 374
                                                                                                                                                                                                                                                                        KTEILLHFVLFDLEHDPLQAGEGDCKYDWLDIWDGIPQVGPLIGRYCGTKMPSDIRSTTG 243
                                                                                                                                                                                                                                                                                                                                        FTSDYARQGAGFSLRYEIYKTGSEDCSRNFTASNGTIESPGFPDKYPHNLDCVFTIIAKP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFLGLCLPGSG----GAAETAQPCGGRLNSKDAGYITSPGYPNDYPSHQNCEWVIYAPEP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00431; CUB; 2.
PF00754; F5_F8_type_C; 2.
PF00629; MAM; 1.
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SM00231; FA58C; 2.
SM00137; MAM; 1.
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IPR000421; FA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               919 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103154 MW; 418AB528D62D59B4 CRC64;
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                                                                                                                                                                                                                                                                                                        -----CPAGCRDV-----AGDISG-----NMVDGYRDTSL 198
430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 102;
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                                                                                                                                                                                                        291
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Search completed: May 15, 2003, 13:18:46
Job time: 75.8563 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Gapop 10.0 ,
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3770
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1: /SIDS2/gcgdata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908470 seqs, 133250620 residues
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1475.448 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score Match Length DB ID  3770 100.0 715 22 AAU00670  2812 74.6 539 22 AAU00630  2812 74.6 586 22 AAU00629  2812 74.6 586 22 AAU00629  2812 74.6 586 22 AAU00629  2812 74.6 586 22 AAU00628  2812 74.6 586 22 AAU0
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
<u>သ</u> သ	335	335	335	335	335	335	335	338.5	338.5	338.5	338.5	341	345.5	349	349	351.5	351.5	351.5	351.5	351.5	351.5	354.5	354.5	354.5	354.5	354.5	354.5	354.5	354.5	362.5	364.5	684.5	692.5	692.5
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923	923	923	856	840	644	600	538	923	923	923	892	439	487	555	439	931	931	931	926	926	909	931	926	914	909	909	909	906	901	925	889	365	385	385
20	20	20	22	22	20	22	22	23	21	20	21	22	22	20	22	20	20	20	23	20	20	20	20	20	21	20	20	20	20	20	21	23	23	23
AAW96246	AAY23247	AAY06317	AAB62478	AAU02949	AAY06319	AAU02948	AAU02950	ABB57098	AAB24213	AAW96248	AAB24215	AAB64628	AAB64570	AAY06320	AAB64627	AAY23248	AAY14563	AAY06318	AAE22718	AAW96255	AAW96254	AAW96253	AAW96252	AAW96251	AAB24214	AAW96250	AAW96249	AAW96257	AAW96256	AAW96308	AAB24216	AAE22721	АВВ97386	AAU79460
Human semaphorin r	Human VEGF165R/NP-	Human neuropilin-1	Human NP-1 recepto		Human soluble neur	Angiotensin conver	~		soluble neu	Mouse semaphorin r	Soluble neuropilli	Human secreted pro		soluble r	secre		VEGF(165)R/		neuropilin-	semaphorin	semaphorin	semaphorin	semaphorin	semaphor	soluble neu	Mouse semaphorin r	emaphorin re	semaphorin		Neuropilin-2. Rat	le neuropill	_	human prote	Human Neuropilin-H

# ALIGNMENTS

RESULT 1 AAU00670

AAU00670 standard; Protein; 715 AA.

Human; TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung; skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer; anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis; attention deficit disorder; Crohn's disease; gastroenteritis; goitre; hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism; muscular dystrophy; immuno-competence; vertebrate; blood; serum.

## Homo sapiens.

XX	FT	Ħ	Ħ	FT	FT	FΤ	FΤ	FT	FΤ	FH	×	8	X	W	3	KΨ	ΚW	X	W	KW	ΚW	×	DE	×	ď	X	Ą	
<pre>/note= "Cytoplasmic domain" xx</pre>	Domain		Domain .	FT /note= "Mature human TANGO 229"	Protein 35715		Domain		Peptide			OS Homo sapiens.				KW attention deficit disorder; Crohn's disease; gastr		anaphylaxis; hepatitis; multiple scle	bone marrow; thymus tissue; abnor	skeletal muscle; kidney; spleen; lymph n	Human; TANGO 229; T cell; heart; liver;		DE Human TANGO 229 polypeptide.		DT 07-SEP-2001 (first entry)	XX ·	AC AAU00670;	
".		ain"		229"		ain"								rtebrate;	riosis; p	se; gastr	ateral sc	s; corona	blood coagula	de; perip	pancreas;							

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents human TANGO 229 polypeptide. This protein and CC similar others exhibit the ability to affect growth, proliferation, cc survival, differentiation, activity, morphology, or movement/migration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, CC brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marvo or thymus tissue. They can be used as condulating agents for regulating cellular processes, thus, the proteins and their associated nucleic acids can be used to prognosticate, prevent, CC diagnose, or treat disorders associated with physiological processes. These disorders include abnormal blood coagulation, asthma, anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohm's disease, gastroenteritis, goltre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immuno-competent vertebrate and harvesting blood or serum from the vertebrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule for diagnosis, therapy of human and other animal disorder, or as
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IVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQITQGNDS
                                                                                SGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNENEYVKSFYMNFKNNNSKWKTYKG
                                                                                                                                                                                            VAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRD
                                                                                                                                                                                                                                                                         LLLNTSEVTVRPESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRD
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                                                                                                                                                                                                                                                                                                                                                                                                     MVPGARGGGALARAAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPG 60
                                                                SGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKG
                                                                                                                                                                                                                                                          LLLNTSEVTVRFESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRD
                                                                                                                                                                                                                                                                                                                       TYPNHTYCEKTITYPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYCGSMTYPKE
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715; Conser
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Pred. No. 1e-306;
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     The sequence represents a novel human protein (NHP) containing a CUB domain (an extracellular domain). CUB proteins have been associated with regulating development, modulating cellular processes and preventing infectious disease. NHP nucleotide sequences are useful for gene therapy of physiological disorders or diseases. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene patterns. NHP nucleotide sequences are useful for detecting mutant or inappropriately expressed NHPs (for example, those proteins associated with obesity, high blood pressure, connective tissue disorders and infertility) for the diagnosis of a disease. The polynucleotides may also be used in screening for drugs effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. Nucleotide constructs encoding NHP products are used to
the body. Nucleotide genetically engineer
                                                                                                                                                                                                          Claim 5; Page
                                                                                                                                                                                                                                                Novel nucleic acid encoding human for drug screening, diagnosis and
                                                                                                                                                                                                                                                                                                        WPI; 2001-290917/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHP-mediated
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                                                                                                                                                                                                                                                                                                                                  Donoho G,
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18-FEB-2000; 2000US-0183583.
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                                              08-OCT-2000; 2000WO-US28798
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                                                                                                             NHP-mediated
                                                                                                                    Novel human protein; NHP; CUB obesity; high blood pressure;
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                     99US-0160285.
2000US-0183583.
                                                                                                             pathway
       GENETICS INC
                                                                                                                                                                                            Protein;
                                                                                                                    pressure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the identification of compounds that bind \ensuremath{\mathsf{NHP}}\xspace-\ensuremath{\mathsf{mediated}}\xspace pathways.
                                                                                                                                           sequence
                                                                                                                                                                                            586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2812; DB 22;
Pred. No. 1.2e-226;
                                                                                                                    domain; extracellular domain; connective tissue disorder; in
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Matches Query Match Best Local :

538;

Similarity

74.6%; ilarity 100.0%; Conservative

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Mismatches

Score 2812; DB 22; Pred. No. 1.4e-226;

Length

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regulating development, modulating cellular processes and preventing infectious disease. NHP nucleotide sequences are useful for gene therapy of physiological disorders or diseases. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene patterns. NHP nucleotide sequences are useful for detecting mutant or inappropriately expressed NHPs (for example, those proteins associated with obesity, high blood pressure, connective tissue disorders and infertility) for the diagnosis of a disease. The polynucleotides may also be used in screening for drugs effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. Nucleotide constructs encoding NHP products are used to genetically engineer host cells to express such products in vivo. These host cells allow for the identification of compounds that bind to NHP receptors or trigger NHP-mediated pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a novel human domain (an extracellular domain). CUB
Sequence
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AA;
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                                                                                                                                                                                                                                                                CC The sequence represents a novel human protein (NHP) containing a CUB CC domain (an extracellular domain). CUB proteins have been associated with CC regulating development, modulating cellular processes and preventing CC infectious disease. NHP nucleotide sequences are useful for gene therapy CC of physiological disorders or diseases. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene CC patterns. NHP nucleotide sequences are useful for detecting mutant or CC inappropriately expressed NHPs (for example, those proteins associated CC with obesity, high blood pressure, connective tissue disorders and CC infertility) for the diagnosis of a disease. The polynucleotides may also CC be used in screening for drugs effective in the treatment of symptomatic CC the body. Nucleotide constructs encoding NHP products are used to CC genetically engineer host cells to express such products in vivo. These CC cost cells allow for the identification of compounds that bind to NHP can be compounded to the compounds that bind to NHP constructs or trigger NHP-mediated pathways.
                                                                                                                                                                                       Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 26; 33pp; English.
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18-FEB-2000;
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                                                                                                                                                                                                  Local
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                       MTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYC 112
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ANGVLSRDGSLSDKRFLFTSNGCSRSLSFEPDGQIRASSSWQSVNESGDQVHWSPGQARL
                                                                                                                                                                                       al Similarity
486; Conserv
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                                                                                                                                                                                      67.7%; Score 2551; DB 22; ilarity 100.0%; Pred. No. 7.9e-205; Conservative 0; Mismatches 0;
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2000US-0183583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pressure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain; extracellular domain;
connective tissue disorder; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUB-domain containing protein, useful treatment of physiological disorders
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infertility;
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                                                                                                                                                                                                   Strachan L,
Murison JG;
                                                                                                                          Polypeptide expressed in mammalian fsn -/- lymph node stromal cells, useful for modulating growth of blood cells, for treating inflammatory and tumour necrosis factor-mediated disorders, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                             blood vessel growth; tumour necrosis factor disorder; arthritis; inflammatory bowel disease; fibroblast growth factor-mediated disorder;
                                                                                                                                                                                                                                                         25-MAR-1999;
26-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                          cardiac
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide isolated from lymph node stromal cells of fsn
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DB; AAA96736.
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99US-0383586.
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The present sequence represents a polypeptide sequence which is isolated from lymph node stromal cells of fsn -/- mice. The polynucleotides and their polypeptides are useful for treating an inflammatory disorder, disorder of immune system and cancer selected from epithelial, lymphoid, mysloid, stromal and neuronal cancers, a viral disorder, in particular HIV infection and for modulating the growth of blood vessels. The polypeptides are useful for treating a

Claim 1; Page

68-69;

75pp;

English

growth of blood tumour necrosis

vessels. The polypeptides are useful factor (TNF) mediated disorder, such

selected

Human neuropilin-Hyl protein

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from arthritis, inflammatory bowel disease and cardiac failure and a fibroblast growth factor-mediated disorder. It is also useful in assay to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, to quantify levels of protein or cognate corresponding ligand or receptors, as antiinflammatory agents, and in compositions for the treatment of skin, connective tissue and immune system diseases. The polynucleotide is useful as marker for tissue, as a chromosome marker or tags in the identification of a genetic disorder.
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 465
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                                                                                                                                                                    EAQKTDCWKQIKYPFARHQSAEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVTR
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L-;-DSRDPASQSQMT-SGGDDGYSAPRNGLAPLNQTAMTALL
                        LATESCHPDSQKPPTHPGTSDSYSAPRDCLTPLNQTAMTALL 715
                                                                                                                                                                                                                                                                                      NFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTSQSTSVS
                                                                                                                                                                                                                                                                                                                                                                                            GCSRSLSFEPDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREW
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                                                                                                      KGSTFRPMDTDTEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPEYATPIVERHLLRAH
                                                                                                                                                       DAQKTGCWKQIKYPFARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVAR
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Pred. No. 2.6e-151;
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RESULT 6
AAE22715
ID AAE2
XX
AC AAE2
XX
DT 09-A
XX

standard;

Protein;

398

8

AAE22715; AAE22715; 09-AUG-2002

(first entry)

Query Match Best Local Similarity

37.4%; 72.8%;

Score 1409.5; DB 23; Pred. No. 2.6e-109;

Length

Sequence

**398** 

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cerebrovascular; stroke; ulcer; immune; infection; multiple sclerosis; human immunodeficiency virus; HIV; autoimmune disorder; dermatological; systemic lupus erythematosus; rheumatoid arthritis; antithyroid; cancer; autoimmune thyroiditis; diabetes mellitus; graft-versus-host disease; myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; nootropic; neuroprotective; vulnerary; anticonvulsant; antiparasitic; cerebroprotective; tranquilliser; virucide; antibacterial; cytostatic; immunosuppressive; chromosome 6q21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to neuropilin-like polypeptide (neuropilin-Hyl and neuropilin-Hyl) and their corresponding nucleic acids. The neuropilin-like polypeptides and polynucleotides are useful in modulating neuronal growth regenerative capacity, treating neurodegenerative diseases, diagnosing and mapping genetic neuronal defects and degenerative diseases like Alzheimer's disease and for treating learning and memory disorders. They are also useful for inducing angiogenesis, neovascularisation, as well as organ growth and development e.g. heart and other tissues. Antagonists of neuropilin-like polypeptides are useful for treating cancers and other malignant diseases. Neuropilin is used to treat platelet disorders e.g. thrombocytopaenia, plastic anaemia and paroxysmal nocturnal haemoglobinuria and is used in nerve tissue growth or
                                                                                                                                                                                                                                                                                                            regeneration, in wound healing, tissue repair and replacement and in healing of bones, incisions and ulcers. Compositions comprising the sequences of the invention are useful for treating diseases of peripheral nervous system e.g. Parkinson's disease, Huntington's disease, Shy-Drager syndrome, amyotrophic lateral sclerosis, and traumatic disorders e.g. spinal cord disorders, head trauma and cerebrovascular diseases e.g. stroke, ulcers, immune deficiencies and immune disorders, infections by hepatitis viruses, human immunodeficiency virus (HIV), herpes viruses, muscoharteria reishmania con malaria son antrimune disorders e.g.
inflammatory eye disease. The gene therapy techniques. The protein. Neuropilin-Hyl gene
                                                                                                                                       mycobacteria, Leishmania spp., malaria spp., autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, autoimmune thyroiditis, diabetes mellitus, graft-versus-host disease, myasthenia gravis and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated human Neuropilin-Hy1 and Neuropilin-Hy2 polypeptides useful for treating neurodegenerative diseases e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-393966/42
N-PSDB; AAD35992.
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06-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disease;
thrombocytopaenia; memory;
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2001US-317902P.
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    The nucleic acids of the invention are used The present sequence is human neuropilin-Hyl ene is located on chromosome 6q21.
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r's disease; learning; angiogenesis;
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Matches

289;

Conservative

Mismatches

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RESULT 7
AAU79459
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                                                                                                                                                                                                                                                                                     Human; neuropilin-Hy1; chromosome 6q21; neuronal growth; nerve regeneration; neurodegenerative disease; hearning disorder; memory disorder; Alzheimer's disease; angiogenesis; neovascularisation; organ growth; nervous system lesion; cancer; cell proliferation; cell differentiation; stem cell growth factor activity; carkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; haematopoiesis; myeloid cell.disorder; lymphoid cell disorders; anaemia; platelet disorder; thrombocytopaenia; liver fibrosis; lung fibrosis; reperfusion; food supplement; DNA microarray.
         New neuropilin-like polypeptides for diagnosing, treating neurological conditions and disorders, inducing angiogenesis and neovascularisation -
                                                             WPI; 2002-351881/38.
N-PSDB; ABK49565.
                                                                                                                                                  11-SEP-2000;
06-SEP-2001;
                                                           N-PSDB;
                                                                                                                                                                                       11-SEP-2001;
                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                         (TANG/) TANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLERASHYLKTEYSK-FCPAGCRDVAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQ 216
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2001US-0659671.
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                                   preventing
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Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl and Hy2 are located on human chromosome 6q21.

Concern neuropilin-Hyl neuropilin-Like proteins and encoding cDNAs are useful concern neuropilin-Like proteins and degenerative diseases like concern neuropilin-Like proteins and lesions, infectious systems, concern neuropilin-Like proteins and cDNAs are also useful as markers for cancers. The neuropilin-Like proteins and lesions caused by toxic substances.

Concern neuropilin-Like proteins and cDNAs are also useful as markers for cancers. The neuropilin-Like proteins and lesions caused by toxic substances.

Concern neuropilin-Like proteins and cDNAs are also useful as markers for cancers. The neuropilin-Like proteins and lesions caused by toxic substances.

Concern neuropilin-Like proteins and cDNAs are useful for regulating cell for regulating cell concern neuropilin-Like proteins and lesions caused by toxic substances.

Concern neuropilin-Like proteins and cell growth factor activity, for inducing proliferation of neural cells, regeneration of nerve and concern neuropilin-Like proteins are useful for regulating cells.

Concern neuropilin-Like proteins and lesions caused by toxic substances.

Concern neuropilin-Like proteins neuropilin-Like proteins are useful neuropility.

Con
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASD
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                                                                                                                                                                SGKTREGSIAAEEEGVPKLYLVIQKQELVQDLVLVATVGCSRSLSFEPDGQIRASSSWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                          YLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYASSDHPDLIT 157
                     VNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQS
NFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKV-RGN
                                                                                VNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQS
                                                                                                                                                                                                                                                   ISVLQRKGISRYEGILANGVLSREFEIFREQLFSSVLFYSWGNTVHAVIELMFPHMIVWH
                                                                                                                                                                                                                                                                                            ISVLQRKGISRYEGILANGVLS--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA antigen.
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                                                                                                                                                                                                          -----FLFTSNGCSRSLSFEPDGQIRASSSWQS
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Pred. No. 2.6e
11; Mismatches
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RESULT 8
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AAY70539

standard; Protein;

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Best Local S
Matches 233
                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a human Factor 8 homologue (F8H), a coagulation cofactor which is selectively expressed in haematopoietic, heart and reproductive tissues. It has haemostatic and cerebroprotective activities. The F8H contains a Factor 5/8 signature and is useful as a therapeutic for treating coagulation related diseases such as haemophilia and stroke. The nucleic acid is useful as such as haemophilia and stroke. The nucleic acid is useful as hybridisation probe and amplification primer for detecting deficiencies in the level of F8H mRNA, for screening F8H gene mutations and for monitoring regulation of gene expression. Fragments of the nucleic acid are also useful as diagnostic probes and primers, and can be used in screening methods such as those using DNA.chips. The present sequence is also useful as a target to screen therapeutically useful modulators
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor 8 homolog polypeptides and nucleic acids encoding them treating coagulation related disorders such as hemophilia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                             the F8H.
                                                                    TSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN 306
                                                                                                                          DGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLF
                                                                                                                                                                             RFESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNMV 190
                                                                                                                                                                                                                                             GKRLILRLGDLDIE-SQTCASDYLLFTS----SSDQYGPYCG-SMTVPKELLLNTSEVTV 130
                 LFMSGIHVSGRGFLASYSVIDKQDLITCLDTASNFLEPEFSKYCPAGCLLPFAEISGTIP
                                                                                                                                                                                                                    GERVRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITL
                                                      KTSGCYGTLGMESGVIADPQITASSVLEWIDHTGQENSWKPKKARLKKPGPPWAAFATDE
                                                                                                          HGYRDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTF
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)B; AAZ51872.
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-YQWLQIDLNKEKKITGIITTGSTMVEHNYYVSAYRILYSDDGQKWTVYREPGVEQD
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                                                                                                                                                                                                                                                                                                                                  669
                                                                                                                                                                                                                                                                           Conservative
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Pred. No.
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|.3e-66;
|es 217;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                      29-SEP-1999;
03-NOV-1999;
                                                                                                                         N-PSDB; AAH34855
                                                                                                                                                     Ruben
                                                                                                                                                                                                                28-SEP-2000;
                                                                                                                                                                                                                                   05-APR-2001
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                      colorectal carcinoma
                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                   03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                    AAG75450;
                                                                                                                                                                                                                                                                                                                                                                    AAG75450 standard; Protein;
                                                                                                                                                                    (HUMA-) HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 TPNVTKDVALAAVLVPVLVMVLTTLILILVCAWHWRNRKKKTEGTYDLPYW----DRAGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
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                                                                                                                                                                                                                                                                                                                                                                                                               DTPKA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                  DRPKA
                                                                                                                                 2001-235357/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTLHQRSTFKP--EEGKEAGYADLDP---YNSPGQEYYHAYAEPLPITGPEYATPIIMDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVTRKGSTFRPMDTDAEEAG-VSTDAGGHYDCPQRAGRHEYALPLAPPEPEYATPIV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERHVLRAHTF SAOSGYRVPGPOPGHKHSLSSGGFSPVAGVGAQDGDYQRPHSAOPADRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKGMKQFLPAKAVDHEETPVRYSSSE--VNHLSPREVT---TVLQADSAEYAQPLVGGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKQIKYPF-----ARHQSAEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPRNSND-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GNDSLVWRKTSQSTSVSTKKEDETITRPI-----PSEET--STGINITT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQ------ITQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGHPTTSVGQPSTSTFKATGNQP------PPL--VGTYNTLLSRTDSCSSAQAQY
                                                                                                                                                     ,MS
                                                                                                                                                                                                                                                                                                                colon
                                                                                                                                                                                                                                                                                                colon
                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                  670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VAIPLVLLVVLVFAGMGIFAAF-----RKKKKKGS---PYGSAEAQKTDC
                                                                                                                                                                                                                                                                                                                 cancer
                                                                                                                                                                                                                 2000WO-US26524
                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LKNTTAPPKIAKGRAPKFTQPLQPRSSNEFPAQTEQTTASPDIRNTTV
                                                                                                                                                                    GENOME SCI INC
                                                                                                                                                                                      990S-0157137.
990S-0163280.
                                                                                                                                                                                                                                                                                                                antigen
                                                                                                                                                                                                                                                                                                colon
                                                                                                                                                   Birse
                                                                                                                                                                                                                                                                                               cancer antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                    583
                                                                                                                                                   Œ,
                                                                                                                                                    Rosen
                                                                                                                                                                                                                                                                                                                 SEQ ID
                                                                                                                                                                                                                                                                                                                 NO:6214.
                                                                                                                                                                                                                                                                                                detection
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AAAI3243 CO AMADIANA MARCHARM AND AND PROTECTIONS (P), where cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The color cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletic

rectifying mutations or deletions

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon

proteins (P), where

Nucleic acids encoding useful for preventing,

4277 human diagnosing

colon cancer-associated polypeptides, and/or treating colorectal cancers -

Claim 11;

Page 7657-7660; 9803pp;

English

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RESULT 10
RABE22716
ID AAE227
XX AAE22
XX AAE22
XX O9-AU
DY 09-AU
DX Human
XX neurc
KW Human
KW chrom
KW corek
KW carek
KW carek
KW humar
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Best Local S
Matches 208
Human; neuropilin-like polypeptide; neuropilin-Hy2; neovascularisation; neurodegenerative disease; Alzheimer's disease; learning; angiogenesis; thrombocytopaenia; memory; platelet; plastic anaemia; antiinflammatory; ophthalmological; paroxysmal nocturnal haemoglobinuria; protozoacide; wound healing; tissue repair; Parkinson's disease; Huntington's disease amyotrophic lateral sclerosis; Shy-Drager syndrome; trauma; spinal cord cerebrovascular; stroke; ulcer; immune; infection; multiple sclerosis; human immunodeficiency virus; HIV; autoimmune disorder; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                        AAE22716 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .B. Pages 666 to 682 and page 7053 of 1 issing at time of publication, meaning EQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRELETSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREWLEIDIGEKKKITGIRTTGSTQSNFNFYYKSFYMNFKNNNSKWKTYKGIVNNEEKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITLLFM 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LILRLGDLDIE-SQTCASDYLLFTS----SSDQYGPYCG-SMTVPKELLLINTSEVTVRFE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKR 79
                                                                                                                                                                                                                                                                                                                                                                                    VTKDVALAAVLVPVLVMVLTTLILILVCAWHWRNRKKKTEGTYDLPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGNKDYHQDVRNXFLPPIIARFIRVNPTQWQQKIAMKMELLGCQFIPKGRPPKLTQPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNMVDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLLLVLLLLLEDAGAQQGDGCGHTVLGPESGTLTSINYPQTYPNSTVCEWEIRVKMGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNSND----LKNTTAPPKIAKGRAPKFTQPLQPRSSNEFPAQTEQTTASPDIRNTTVTPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GNDSLVWRKTSQSTSVSTKKEDETITRPI-----PSEET--STGINITT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YQWLQIDLNKEKKITGIITTGITMVEHNYYVSAYRILYSDDGQKWTVYREPGVEQDKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCYGTLGMESGVIADPQITASSVLEWTDHTGQENSWKPKKARLKKPGPPWAAFATDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTFKTS
                                                                                                                                                                           neuropilin-Hy2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        -VAIPLVLLVVLVFAGMGIFAAF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                          Protein; 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
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Pred. No. 1
                                                                                                                                                                                                                                                                                          ₽
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g no
                                                                                                                                                                                                                                                                                                                                                                                                                          RKKKKKGS---PY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence listing were 
sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                          490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                           disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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                                       cord;
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Ϋ́O

20

LALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKR

Query Match Best Local S Matches 163

Similarity

18.4%;

Conservative

65;

Indels Length

31;

Gaps

13;

Score 692.5; Pred. No. 3e-4 55; Mismatches

No. 3e-49;

B

385

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systemic lupus erythematosus; rheumatoid arthritis; antithyroid; cance autoimmune thyroiditis; diabetes mellitus; graft-versus-host disease; myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; nootropic; neuroprotective; vulnerary; anticonvulsant; antiparasitic; cerebroprotective; tranquilliser; virucide; antibacterial; cytostatic
                                                         autoimmune pulmonary inflammation, autoimmune thyroiditis, diabetes mellitus, graft-versus-host disease, myasthenia gravis and autoimmun inflammatory eye disease. The nucleic acids of the invention are use gene therapy techniques. The present sequence is human neuronilin-use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth regenerative capacity, treating neurodegenerative diseases, diagnosing and mapping genetic neuronal defects and degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 128-130; 152pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human Neuropilin-Hyl and Neuropilin-Hyl polypeptides useful for treating neurodegenerative diseases e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-2000;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuropilin-Hy2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYSEQ
                                     techniques. The present sequence is human neuropilin-Hy2 ropilin-Hy2 gene is located on chromosome 6q21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0659671.
2001US-317902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US28488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relates to neuropilin-like polypeptide (neuropilin-Hyl
₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Signal_peptide 61..385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nd their corresponding nucleic acids. The neuropilin-
and polynucleotides are useful in modulating neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human mature neuropilin-Hy2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6q21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                            nerve regeneration; neurodegenerative disease; learning disorder; memory disorder; Alzheimer's disease; angiogenesis; neovascularisation; organ growth; nervous system lesion; center; cell proliferation; cell differentiation; stem cell growth factor activity; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; haematopolesis; myeloid cell disorder; lymphoid cell disorders; anaemia;
New neuropilin-like polypeptides treating neurological conditions
                                       WPI; 2002-351881/38
N-PSDB; ABK49567.
                                                                                                                               11-SEP-2000;
06-SEP-2001;
                                                                                                                                                                      11-SEP-2001;
                                                                                                                                                                                                                         W0200222780-A2
                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU79460 standard;
                                                                                                                                                                                               21-MAR-2002.
                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU79460;
                                                                                                      (TANG/)
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       reperfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVEQDKIFQGNKRIITRMVRNNFLPPIIAR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDTSLLCKAAIHAGIIADELGGQISYLQRKGISRYEGILANGYLSRDGSLSDKRFLFTSN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNMVDGY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILRLGDLDIE-SQTCASDYLLFTS----SSDQYGPYCG-SMTVPKELLLNTSEVTVRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNNEEKVFQGNSN-FRDPVQNNFIPPIVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNHKPREWLEIDLGEKKKITGIRTTGSTQ-SNFNFYVKS---FVMNFKNNNSKWKTYKGI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCYGTLGMESGGD-RGSSNNSITVLEW--TDHTGQENSWKPKKSQAE---KTWTALGAFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCSRSLSFEPDGQIRASSS------WQSVNESGDQVHWSPGQARLQDQGPSW-ASGDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGIHVSGRGFLASYSVIDKQDLITCLDTASNFLEPEFSKYCPAGCLLPFAEISGTIPHGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITLLFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLLLVLLLLEDAGAQQGDGCGHTVLGPESGTLTSINYPQTYPNSTVCEWEIRVKMGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTFKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropilin-Hy2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuropilin-Hy2; chromosome 6q21; neuronal growth;
                                                                                                       TANG
                                                                                                                                                                                                                                                                                                                                                                     disorder;
                                                                                                                               2000US-0659671.
2001US-0659671.
                                                                                                                                                                       2001WO-US28590
                                                                                                                                                                                                                                                                                                                                                        food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                        ×
                                                                                                                                                                                                                                              /label= Signal_peptide
21..385
/label= Mature_neuropilin_Hy2
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       supplement;
                                                                                                                                                                                                                                                                                                                                                       thrombocytopaenia; liver fibrosis; lung supplement; DNA microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
for diagnosing, and disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390
 cancers, and
             preventing
                                                                                                                                                                                                                                                                                                                                                                    fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298
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Qy
                                                                                    Matches
                                                                                                                          Best
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                  diseases, and neuropathles, such as Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, to regulate haematopoiesis and treat myeloid and lymphoid cell disorders, various anaemias, and platelet disorders, such as thrombocytopaenia, regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and as a food supplement or molecular weight marker. The cDNAS are useful in gene identification, genome mapping, transgenics, as hybridisation probes, for primer design, for gene chips and as a DNA antigen. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative diseases, learning and memory disorders, diagnosing an mapping genetic neuronal defects and degenerative diseases like Alzheimer's disease, for inducing angiogenesis, and neovascularisation and organ growth and development (e.g. the heart). The nervous systems disorders include lesions of central or peripheral nervous systems, including traumatic lesions, ischaemic lesions, infectious lesions, including traumatic lesions, schaemic lesions, infectious lesions, degenerative lesions, lesions associated with nutritional diseases or disorders, neurological lesions, and lesions caused by toxic substances. The neuropilin-like proteins and cDNAs are also useful as markers for cancers. The neuropilin-like proteins are useful for regulating cell proliferation, cell differentiation, stem cell growth factor activity, for inducing proliferation of neural cells, regeneration of nerve and brain tissue, for treatment of central and peripheral nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated neuropilin-like polypeptide including neuropilin-Hyl and neuropilin-Hy2, the full length cDNAs encoding the proteins and the coding compose of the cDNAs. Also incide a nucleic acid array comprising the cDNAs attached to a surface for detecting full-matches or mismatches to the cDNAs. The genes for neuropilin-Hyl and Hy2 are located on human chromosome 6q21. The nucleic acid array is useful for detecting full-matches or mismatches or mism
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in modulating neuronal growth, regenerative capacity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the cDNAs. The neuropilin-like proteins and encoding cDNAs are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inducing angiogenesis and neovascularisation
    20 LALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKR
                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                         385
                                                                                        Conservative
                                                                                                                                                                                                                                                         A
                                                                                                                          18.4%;
                                                                                        65;
                                                                                                                      Score 692.5; DB 23; Pred. No. 3e-49;
                                                                                        Mismatches
                                                                                        131;
                                                                                        Indels
                                                                                                                                                                Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating
                                                                                    31;
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                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  included
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Q. 밁 Š γQ 밁 밁 Ş 밁 δÃ 밁 밁 Ş 353 362 299 245 254 185 125 134 194 65 80 LILRIGDIDIE-SQTCASDYLLFTS----SSDQYGPYCG-SMTVPKELLLINTSEVTVRFE 133 G VNNEEKVFQGNSN-FRDPVQNNFIPPIVAR 390 NNHKPREWLEIDLGEKKKITGIRTTGSTQ-SNFNFYVKS---FVMNFKNNNSKWKTYKGI GCSRSLSFEPDGQIRASSS------WQSVNESGDQVHWSPGQARLQDQGPSW-ASGDSS RDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLFTSN SGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNWVDGY VRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITLLFM 124 **VVEQDKIFQGNKRIITRMVRNNFLPPIIAR** RDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTFKTS SGIHVSGRGFLASYSVIDKQDLITCLDTASNFLEPEFSKYCPAGCLLPFAEISGTIPHGY GCYGTLGMESGGD-RGSSNNSITVLEW--TDHTGQENSWKPKKSQAE---KTWTALGAFA 382 184 193 64 305 244

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. in burn treatment, to regulate the immune system e.g. to trent inultiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tag (ESTs). They can be used to stimulate cell growth, to regulate haematopolesis e.g. to treat aplastic anaemia, to help tissue regrowth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stroke and cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200222660-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinfertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB97386 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2001; 2001WO-US26015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB97386;
     245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                G
                                                                                                                                                                                            SGIHVSGRGFLASYSVIDKQDLITCLDTASNFLEPEFSKYCPAGCLLPFAEISGTIPHGY
                                                                                                                                                                                                                                                                                                                                                                                                                                            LALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ke and cancer, to screen for drugs, to treat inflammatory conditions rheumatoid arthritis, and to treat nervous system disorders e.g. inson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-292408/33.
                                                                                                                                                                                                                                                                                               VRIKEGDEDIEDSDSCHENYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITLLEM
                                                                                                                                                                                                                                                                                                                                             LILRIGDLDIE-SQTCASDYLLFTS----SSDQYGPYCG-SMTVPKELLLNTSEVTVRFE 13:
                                                                                                                                                                                                                                                                                                                                                                                              LLLLLVLLLLLEDAGAQQGDGCGHTVLGPESGTLTSINYPQTYPNSTVCEWEIRVKMGER 64
GCYGTLGMESGGD-RGSSNNSITVLEW--TDHTGQENSWKPKKSQAE---KTWTALGAFA
                                             GCSRSLSFEPDGQIRASSS------WQSVNESGDQVHWSPGQARLQDQGPSW-ASGDSS
                                                                                                                                         RDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLFTSN
                                                                                                                                                                                                                                            SGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNMVDGY 193
                                                                                              RDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTFKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antianaemic; vulnerary; antiinflammatory; immunomodulator;
fertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN32572
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P, A
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 692.5; DB 23; Pred. No. 3e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ħ
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298
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AAE22
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                                             diagnosing and mapping genetic neuronal defects and degenerative diseases like Alzheimer's disease and for treating learning and memory disorders. They are also useful for inducing angiogenesis, neovascularisation, as well as organ growth and development e.g. heart and other tissues. Antagonists of neuropilin-like polypeptides are useful for treating cancers and other malignant diseases. Neuropilin is used to treat platelet disorders e.g. thrombocytopaenia, plastic anaemia and paroxysmal nocturnal haemoglobinuria and is used in nerve tissue growth or regeneration, in wound healing, tissue repair and replacement and in
                                                                                                                                                                                                                                                                                                                                                               Novel isolated human Neuropilin-Hyl and Neuropilin-Hyl polypeptides useful for treating neurodegenerative diseases e.g. Alzhelmer's disease, and for diagnosing and mapping genetic neuronal defects -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebrovascular; stroke; ulcer; immune; infection; multiple sclerosis; human immunodeficiency virus; HIV; autoimmune disorder; dermatological; systemic lupus erythematosus; rheumatoid arthritis; antithyroid; cancer autoimmune thyroiditis; diabetes mellitus; graff-versus-host disease; myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; noottopic; neuroprotective; vulnerary; autionvulsant; antiparasitic;
                                                                                                                                                                                                                           neuropilin-Hy2) and their corresponding nucleic acids. The neuropilike polypeptides and polynucleotides are useful in modulating neuroweth regenerative capacity, treating neurodegenerative diseases,
                                                                                                                                                                                                                                                                                       The invention relates to neuropilin-like polypeptide (neuropilin-Hyl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2000;
06-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amyotrophic lateral sclerosis; Shy-Drager syndrome; trauma; spinal cord; cerebrovascular; stroke; ulcer; immune; infection; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopaenia; memory; platelet; plophthalmological; paroxysmal nocturnal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; neuropilin-like polypeptide; neuropilin-
neurodegenerative disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE22721;
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                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wound healing; tissue repair; Parkinson's disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human neuropilin-Hy2 mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2002
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                              of bones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYSEQ INC
              of.
                                                                                                                                                                                                                                                                                                                                Page 131-132;
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2001US-317902P.
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          vound measure. Co
incisions and ulcers. Co
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                                                                                                                                                                                                                                                                                                                              152pp;
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                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuropilin-Hy2; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     's disease; learning; anglogenesis; plastic anaemia; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemoglobinuria;
Compositions compre-
                                                                                                                                                                                                                                                                    acids. The neuropilin-
                            comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protozoacide;
                                                                                                                                                                                                                                                  neuronal
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                           Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory eye disease. The nucleic acids of the invention are used gene therapy techniques. The present sequence is human neuropilin-Hy2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome, amyotrophic lateral scierosis, and traumatic disorders e.g. spinal cord disorders, head trauma and cerebrovascular diseases e.g. stroke, ulcers, immune deficiencies and immune disorders, infections by
                      (KAGA-) KAGAKU
                                                                             17-FEB-1999;
                                                                                                                                   17-FEB-1999;
                                                                                                                                                                                          05-SEP-2000
                                                                                                                                                                                                                                             JP2000236879-A.
                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                 Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Soluble neuropillin sNP-2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB24216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB24216 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                      GIJUTSU SHINKO JIGYODAN
                                                                             99JP-0038920
                                                                                                                                   99JP-0038920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human bioreactions and disease conditions. The present sequence represents a specifically claimed soluble neuropillin protein sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant soluble neuropillin (I) comprising an amino acid sequence in which the cell membrane-penetrating region and/or the intracellular region is deleted from a mouse-derived neuropillin. The soluble neuropillin can be used for the elucidation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble neuropillin having a used to diagnose human diseas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VPGARGGGALARAAGRGLLALLLAVSAPLRLQAEELGD-GCGHLVTYQDSGTMTSKNYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STNGEDWAYZRHGKNH--KIFQANNDATEVVLNKLHMPLLTRFIRIRPQTWHLGIALRLE
SKPTVETLGPTVKSEETTTPYPMDEDATECG
                                                    YQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG
                                                                                                                                                                 QIKYPFARHQSA-EFTISYD-------NEKEMTQKLDLITSDMAD
                                                                                                                                                                                                                        GEEW-LQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVRKFKVSYSLNGKD-----WE
                                                                                                                                                                                                                                                                          SEETSTGINITTVAIPLVLLVVLVFAGMGIFA----AFRKKKKKGSPYGSAEAQKTDCWK
                                                                                                                                                                                                                                                                                                                                  LFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSPSAARLVSSRSGWFPRNPQAQP
                                                                                                                                                                                                                                                                                                                                                                                          LIGCOITOGNDSLVWRKTS---QSTSVSTKKEDETITRPI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQGAISRETQKGYYVKSYKLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIANEQISASSTFSDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYLIHQEPPENFQCNVPLGMESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --HPDLITC----LERASHYLKTEYSKF-------CPAGCRDVAGDIS--GNMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGSEDCSKNFTSPNGTIESPGFP
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                                                                                                            YIQDPRTQQTKLFEGNMHYDTPDIRRFDPVPAQYVRVYPERWSPAGIGMRLEVLGCDWTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSFVMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKYPHNLDCTFTILAKPRMEIILQFLTFDLEHDPLQVGEGDCKYDWLDIWDGIPHVGPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnose human disease conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          889 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 364.5; DB Pred. No. 3.3e-21 Pred. No. 3.2e-21 Pred. No. 3.2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- QPARRAVRSLQDPPCGGRPNSKDAGYITSPGYPQ
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                              correct sensory afferent innervation and other aspects of development. Agents which inhibit or enhance the interaction of a semaphorin and a neurophilin can be potent modulators of nerve cell growth, immune responsiveness, and viral pathogenesis, and can be used in the treatment and diagnosis of neurological disease, neuro-regeneration, immune modulation including hypersensitivity and graft-rejection, and diagnosis and treatment of viral and oncological infection/diseases. The neuropilins, neuropilin-encoding nucleic acids, and unique portions also are useful in screening chemical libraries for regulators of semaphorin-mediated cell activity, and in genetic mapping as probes for related genes, as diagnostic reagents for genetic, neurological, immunological and oncological disease.
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The neuropilins are type I transmembrane proteins and act as semaphorin III (Sema III) receptors. The semaphorins have been shown to function in repulsive axon guidance. Sema III is a secreted protein that in vitro causes neuronal growth cone collapse and chemorepulsion on neurites and is regulared in vivo for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropilin; neuropilin-2; semaphorin; transmembrane proteineurone; development; cell growth; imunne response; viral pathogenesis; treatment; disease; graft rejection; viral disease; oncological disease; cancer; screening; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Page 77-79; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated semaphorin receptor, neuropilin-2 - used to develop products for the diagnosis and treatment of neurological, immunological, oncological and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-132446/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ginty DD, Kolodkin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX08417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuropilin-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW96308
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174 -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRY--
                                           147
                                                                               150
                                                                                                                                                                                                                 41 CGHLVTYQDSGTMTSKNYPGTYPNHTYCEKTITYPK-GKRLILRLG-DLDIESQTCASDY 98
                                                                                                                  88
                                                                                                                                                        99
                                                                                                                                                                                            28
                                                                                                                IEIRDGDSESADLLGKHCGNI-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGS 146
                                                                                                                                                      LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS 149
                                                                                                                                                                                            CGGRLNSKDAGYITSPGYPQDYPSHQNCEWVVYAPEPNQKIVLNENPHFEIEKHDCKYDF 87
                                                                               SD-----
                                       EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPRMEIIIQFLTFDLEHDPLQVGEG 206
                                                                                                                                                                                                                                                                                                                                                  925 AA;
                                                                                                                                                                                                                                                                         Conservative 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  970S-0052762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oncological disease; cancer; screening; probes
                                                                                                                                                                                                                                                                       9.6%; Score 362.5; DB 20; 22.3%; Pred. No. 5.2e-21; ative 100; Mismatches 246;
                                                                             -----HPDLITC----LERASHYLKTEYSKF--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane protein; axon;
                                                                                                                                                                                                                                                                     246; Indels 151; Gaps
                                                                                                                                                                                                                                                                                                        Length 925;
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Search completed: May 15, 2003, 13:20:42 Job time: 68.5731 secs

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US-09-759-130B-78

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US-10-104-440-4

2 US-10-104-440-2

2 US-10-115-563-14

4 US-10-195-718-4

US-10-190-593-2

US-10-190-593-2

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US-10-003-132-6
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US-10-003-132-2
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US-10-003-132-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 2001-11-15

PRIOR ETLING DATE: 2000-11-15

NUMBER OF CENTRE 2000-11-15
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FILE REFERENCE: 00-62
CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15

SOFTWARE: FastSEQ for Windows Version 3.0

NUMBER OF SEQ ID NOS:

APPLICANT: Gao, Zeren
APPLICANT: Shoemaker, Kimberly E.
TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCUB5

APPLICANT: Fox, Brian A. APPLICANT: Gao, Zeren APPLICANT: Shoemaker, K.

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US-09-874-198-2	US-09-900-518A-2	US-09-770-643A-28	US-09-770-643A-24	US-09-770-643A-2	US-09-770-643A-4	US-09-770-643A-20	US-09-770-643A-22	US-09-770-643A-16	US-09-770-643A-18	US-09-770-643A-12	US-09-770-643A-14	US-09-770-643A-10	US-09-770-643A-8	US-09-996-015-9	US-10-238-876-2	US-09-996-015-11	US-10-238-876-8	US-09-996-015-10	US-10-187-319-37	US-10-187-319-39	US-10-187-319-6	US-10-132-829-4	US-10-187-319-2	US-09-957-641-2	US-10-095-718-2
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## ALIGNMENTS

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Best Local Similarity
Matches 715; Conserv
 181
                                                      181 VAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRD
                                                                                                                61 TYPNHTYCEKTITYPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYCGSMTYPKE 120
61 TYPNHTYCEKTITYPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYCGSMTYPKE 120
                                                                                                                                                                           1 MYPGARGGGALARAAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPG
VAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRD
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Sequence 73, Application US/09759130B
Publication No. US20030022279A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Ir
APPLICANT: MCCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
        APPLICANT: WILGHTON, NICOLAS
APPLICANT: GOODEATI, ANDREW
APPLICANT: HOLTZMAN, DOUGLAS A
TITLE OF INVENTION: NOVEL GENES ENCODING PROT
TITLE OF INVENTION: NOVEL GENES ENCODING PROT
TITLE OF INVENTION: USES.
FILE REFERENCE: MPIOO-5350MNIM
CURRENT APPLICATION NUMBER: US/09/759.130B
CURRENT FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-19
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR APPLICATION NUMBER: US 09/303,996
PRIOR APPLICATION NUMBER: US 09/303,996
PRIOR APPLICATION NUMBER: US 09/303,996
PRIOR APPLICATION NUMBER: US 09/393,996
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Fraser, Christopher C
Sharp, John D
Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Myers, Paul S
Leiby, Kevin R
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                                                                RESULT 3
US-09-759-130B-75
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Sequence 75, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, APPLICANT: McCarthy, Sean A APPLICANT: Fraser, Christopher C APPLICANT: Sharp, John D
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Best Local S
Matches 715
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Pred. No. 8e-284;
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McCarthy, Sean A Fraser, Christopher Sharp, John D

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NUMBER OF SEQ ID NO:
SOFTWARE: FastSEQ fo
SEQ ID NO 75
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Best Local S
Matches 681
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ORGANISM: Homo sapiens
-09-759-130B-75
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TITLE OF INVENTION: NOVEL GENES E
TITLE OF INVENTION: PROGNOSTIC,
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
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APPLICATION NUMBER: US 09/559,497

R FILING DATE: 2000-04-27

APPLICATION NUMBER: US 09/578,063

R FILING DATE: 2000-05-24
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APPLICATION NUMBER: US 09/602,871
FILING DATE: 2000-06-23
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FILING DATE: 1999-06-14
APPLICATION NUMBER: US 09/596,194
FILING DATE: 2000-07-14
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FILING DATE: 1999-06-29
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                                                                      SNENEYVKSEVMNEKNNNSKWKTYKGIVNNEEKVEQGNSNERDPVQNNEIPPIVARYVRV
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                                                                                                                           SVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQ
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US-09-759-130B-76
                                        NUMBER: FASE
SOFTWARE: FASE
SEQ ID NO 76
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Publication No.
                                                                                                                                                                                                                                                                                                                                          PRIOR AFFILING DATE: 2000-04-2,
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR AFFILING DATE: 2000-05-24
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PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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FILE REFERENCE: MP100-5350MNIM
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APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
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PRIOR FILING DATE: 1999-06-14
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                                                                                                                               APPLICATION NUMBER: US FILING DATE: 2000-06-23 APPLICATION NUMBER: US
                                                                                                                                                                                   APPLICATION NUMBER: US (FILING DATE: 1999-09-10
                                                                                                                                                                                                                   APPLICATION NUMBER: US (FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/342,364 FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/596,194 FILING DATE: 2000-07-14
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Goodearl, Andrew
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Myers, Paul S
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Kirst, Susan
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                                                                                 for
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                                                                                                                                                                 09/602,871
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US-10-003-132-4
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US-10-003-132-4
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PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 19
SOPTWARE: FASTSEQ for Windows Version 3
SEQ ID NO 4
LENGTH: 503
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10003132 Publication No. US20020192750A1 GENERAL INFORMATION:
                                                                                                                           Query Match
Best Local Similarity
Matches 392; Conserv
                                                                                                                                                                                                                                                                     APPLICANT: FOX, Brian A.
APPLICANT: GAO, Zeren
APPLICANT: Shoemaker, Kimberly E.
TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCU
FILE REFERENCE: 00-62
CURRENT PEPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15
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                                                                                                                                     51.0%;
                                                                                                                            34;
                                                                                                                          Score 1924.5; DB 9;
Pred. No. 5.9e-141;
34; Mismatches 73;
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                                                                                                                                                DB 9;
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VPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFE
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NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 51
LENGTH: 503
TYPE: PRT
ORGANISM: Mouse
US-09-823-038A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51, Application U
Patent No. US20020058335Al
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Mevin
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions isolated From Stromal Cells
FILE REFERENCE: 11000.1037c3
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/823,038A CURRENT FILING DATE: 2001-07-09
                                          14 AAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTIT 73
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TFSTQSGYRVPGPRPTHKHSHSSGGFPPATG-ATQVESYQRPASPKPVGGGYDKPAASSF
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                                                                                       Conservative
                                                                                                           50.7%;
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                                                                                       35;
                                                                                  Score 1912.5; DB 10
Pred. No. 5e-140;
35; Mismatches 74;
                                                                                                                             DB 10;
                                                                                       Indels
                                                                                                                               Length 503;
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US-10-003-132-6
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APPLICANT: FOX, Brian A.
APPLICANT: Gao, Zeren
APPLICANT: Shoemaker, Kimberly E.
TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCUB5
FILE REFERENCE: 00-62
                                                          Query Match
Best Local :
                                                                                                                             SEQ ID NO 6
LENGTH: 458
                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10003132 Publication No. US20020192750A1
                                               Matches
                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/249,004
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                   TYPE: PRT
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                                                           Similarity
                                               Conservative
                                                                                                       musculus
                                                         44.88;
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                                             Score 1690; D
Pred. No. 7.8e
31; Mismatches
                                              ; DB 9;
7.8e-123;
hes 69;
                                                                 Length
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                                               248;
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; Sequence 78; Application US/09759130B

; Publication No. US20030022279A1
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APPLICANT: Millennium Pharmaceuticals,
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APPLICANT:
APPLICANT:
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APPLICANT:
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
                                                                   FILE REFERENCE: MPIO0-5350MNIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
                                                                                                          APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES;
TITLE OF INVENTION: PROGNOSTIC,
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                 APPLICANT:
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Fraser, Christopher C
Sharp, John D
Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Frathy France
                                                                                                                                                                                              Leiby, Kevin R
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|-TTPGMNITTVAIPSVIFIALLLTGMGIFAICRKRKKGNPYVSA
                                                                                                                         ENCODING PROTEINS HAVING , DIAGNOSTIC, PREVENTIVE,
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OTHER

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RESULT 9
US-10-060-830-3
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SOFTWARE: FastSEQ
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10060830 Publication No. US20030032154A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 33.6%;
Best Local Similarity 100.0%;
Matches 235; Conservative
                                                                                                                                                                                            PRIOR PRIOR
                                                                                                                                                                                                                               PRIOR PRIOR
                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/060,830
CURRENT FILING DATE: 2002-01-30
                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                              PRIOR
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PB0169
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
                                                                                                                                                           PRIOR
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                                    PRIOR FILING DATE:
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                       APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                  APPLICATION NUMBER: US 60/325,062 FILING DATE: 2001-09-25
                                                                    APPLICATION NUMBER: US 09/864,761 FILING DATE: 2001-05-23
                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00669
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NUMBER: US 09/393,996
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NUMBER: US 09/333,159
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Best Local Sim
Matches 263;
                                                                                Sequence 1114, Application US/10060830 Publication No. US20030032154A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
LENGTH: 729
                       APPLICANT: Gu, Yizhong
APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
                  FILE REFERENCE:
                                                                                                                                                                                                            069
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                                                                                                                                                                                                                                                                                                                                                                                                                       MKQFLPAKAVDHEETPVRYSSSE--VNHLSPREVT---TVLQADSAEYAQPLVGGIVGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTKDVALAAVLVPVLVMVLTTLILILVCAWHWRNRKKKTEGTYDLPYW----DRAGWWKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNSND----LKNTTAPPKIAKGRAPKFTQPLQPRSSNEFPAQTEQTTASPDIRNTTVTPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTFKTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLLLVLLLLLEDAGAQQGDGCGHTVLGPESGTLTSINYPQTYPNSTVCEWEIRVKMGER
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                                                                                                                                                                                                                                                                                  PTTSVGQPSTSTFKATGNQP--
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 APPLICATION
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NUMBER: US/10/060,830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113; Mismatches 240;
                                                                                                                                                                                                                                                                                  -PPL--VGTYNTLLSRTDSCSSAQAQYDTP
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US-10-060-830-1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.2%; Score 873.5; DB 9; Best Local Similarity 35.1%; Pred. No. 2.6e-59; Matches 224; Conservative 102; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1123
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 1114
LENGTH: 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/325,062 PRIOR FILING DATE: 2001-09-25
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                                                                                                                                  576 GHYDCPQRAGRHEYALPLAPPEPEYATPIV---ERHVLRAHTFSAQSGYRVPGPQPGHKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
                                                                                                                                                                                                                         517 TISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVTRKGSTFRPMDTDAEEAG-VSTDAG
                                                                                                                                                                                                                                                                      425 ILVCAWHWRNRKKKTEGTYDLPYW----DRAGWWKGMKQFLPAKAVDHEETPVRYSSSE-
                                                                                                                                                                                                                                                                                                                                                                365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 CLERASHYLKTEYSKFCPAGCRDVAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 VVPQTWHQRIALKVELIGCQ-----ITQ-----GNDSLVWRKTSQSTSVSTKKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 SYLQRKGISRYEGILANGYLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSW 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 LLLEDAGAQQGKYCGLGLQMNHSIESKGNEITLLFWSGIHVSGRGFLASYSVIDKQDLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 CLDTASNFLEPEFSKYCPAGCLLPFAEISGTIPHGYRDSSPLCMAGVHAGVVSNTLGGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 LLFTSSSDQYGPYCG-SMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYASSDHPDLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 09/864,761
FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                PKFTQPLQPRSSNEFPAQTEQTTASPDIRNTTVTPNVTKDVALAAVLVPVLVMVLTTLIL
                                                                                                                                                                                                                                                                                                                                                                                                        ETITRPI------PSEET--STGINITT-----VAIPLVLLVVLVFAGMGIFA
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                                          SLSSGGFSPVAGVGAQDGDYQRPHSAQPADRGYDRPKA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVVISKGIPYYESSLANNVTSVVGHLSTSLFTFKTSGCYGTLGMESGVIADPQITASSVL 192
                                                                                       --- YNSPGQEVYHAYAEPLPITGPEYATPIIMDMSGHPTTSVGQPSTSTFKATGNQP----
                                                                                                                                                                                 -VNHLSPREVT---TVLQADSAEYAQPLVGGIVGTLHQRSTFKP--EEGKEAGYADLDP-
PPL--VGTYNTLLSRTDSCSSAQAQYDTPKA 615
                                                                                                                                                                                                                                                                                                                 ---RKKKKKGS---PYGSAEAQKTDCWKQIKYPF-----ARHQSAEF
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; ORGANISM: human
US-10-104-440-4
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US-10-104-440-4
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Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10104440 Patent No. US20020132774A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/104,440 CURRENT FILING DATE: 2002-03-22 PRIOR APPLICATION NUMBER: 09/580,803 PRIOR FILING DATE: 2000-05-30 PRIOR APPLICATION NUMBER: 60/069,155 PRIOR FILING DATE: 1997-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/069,687 PRIOR FILING DATE: 1997-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTAGONISTS OF NEUROPILIN RECEPTOR FUNCTION AND USE TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KLAGSBRUN, Michael APPLICANT: SOKER, Shay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/078,541 PRIOR FILING DATE: 1998-03-19
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                                                                                                         447
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                                 405 LKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP------IP
                                                                                                                                                                                                                                                                                                                                                                                       231 ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 IEIRDGDSESADLLGKHCGNI-APPTIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF
                                                                                                                                                                                                                                                                               SEETSTGINITTVAIPLVLLVVLVFAGMG---IFA----AFRKKKKKGSPYGSAEAQKTD
                                                                                                                                                                                                                                                                                                                                                       FSARYYLVHQEPLENFQ-----CNVPLGMESGRIANEQISASSTY-----
                                                                    QAQPGEEWLQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVRKFKVSYSLNGKD-----
                                                                                                                                                                                                                                                VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA 404
                                                                                                                                                                                                                                                                                                                                                                                                                            DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAK------DG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY----AS
                                                                                                                                        LRLELFGCRVTDAPCSNMLGMLSGLIADSQISASSTQEYLWSPSAARLVSSRSGWFPRIP
-WEYIQDPRTQQPKLFEGNMHYDTPDIRRFDPIPAQYVRVYPERWSPAGIGMRLEVLGCD
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MIAO, Hua Quan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 351.5; DB 12; 22.2%; Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.0
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WTD-SKPTVETLGPTVKSEETTTPYPTEEE----ATECG 627

MADYQOPLMIGTGTVTRKGSTFRPMDTDAEEAGVSTDAG 575

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; LENGTH: 923
; TYPE: PRT
; ORGANISM: human
US-10-104-440-2
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US-10-104-440-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/104,440 CURRENT FILING DATE: 2002-03-22 PRIOR APPLICATION NUMBER: 09/580,803 PRIOR FILING DATE: 2000-05-30 PRIOR APPLICATION NUMBER: 60/069,155 PRIOR FILING DATE: 1997-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KLAGSBRUN, Michael
APPLICANT: SOKER, Shay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ANTAGONISTS OF NEUROPILIN RECEPTOR FUNCTION AND USE TITLE OF INVENTION: THEREOF FILE REFERENCE: 48802 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SOKER, Shay
APPLICANT: MIAO, Hua Quan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/069,687
PRIOR FILING DATE: 1997-12-29
PRIOR APPLICATION NUMBER: 60/078,541
PRIOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                              307
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                                                                                                                                                                                                                                                                                                                                                                                                               176 IVFAPKMSEIILEFESFDLEPDSNP--PGGMFCRYDRLEI----WDGFPD-----VGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 GPFLFIKFVSDYETHGAGFSIRYEIFKRGPECSQNYTTPSGVIKSPGFPEKYPNSLECTY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 RGL-----LALLLAVSAPLRLQAEELGDGCGHLYTYQDSGTMTSKNYPGTYPNHTVCEK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 LIQAPDPYQRIMINFNPHFDLEDRDCKYDYVEVFDGENENGHFRGKFCGKI-APPPVVSS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 TITVPKG-KRLILRLG-DLDIESQTCASDYL-LFTSSSDQ---YGPYCGSMTVPKELLLN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RGLPLLCAVLALVLAPAGAFR-----NDKCGDTIKIESPGYLTSPGYPHSYHPSEKCEW 56
LVWRKTSQSTSVSTKKED 438
                                                          KPVLEQGNINPIDVVVAVEPKPLITREVRIKPATWETGISMRFEVYGCKITDYPCSGMLG 436
                                                                                                                                                                                                                                                                                TSNGCSRSLSFEP----DGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN 306
                                                                                                                                                 ----REWIQVDLGLLREVTAVGTQGAISKETKKKYYVKTYKIDVSSNGEDWITIK--EGN
                                                                                                                                                                                         NHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNN 364
                                                                                                                                                                                                                                       ----CMEALGMESGETHSDQITASSQYST-----NWSAERSRLNYPENGWTPGEDSY
                                                                                                                                                                                                                                                                                                                             IGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVLQSSV-SEDFK-----
                                                                                                                                                                                                                                                                                                                                                                      AG-IIADELGGQI------SVLQRKGISRYEGILANGVLSRDGSLSDKRFLF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LERASHYLKTEYSKFCPAG--CRDVAGDISGNMVDGYRDTSLLCKAAIH 205
                                                                                                   EEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQIT----QGNDS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124;
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24.9%; Pred. No. 2.4e-17;
ative 76; Mismatches 176;
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US-10-095-718-4
; Sequence 4, Application US/10095718
; Patent No. US20020131956A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Christopher

RESULT 14

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US-10-115-563-14
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                                                                                                                                                                                                                                             Query Match 8.4%;
Best Local Similarity 42.0%;
Matches 71; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
        2175
                                                                                                                                                                 2064 NGCSTPLGMENGKIENKQITASSFKKSWW-----GD--YWEPFRARLNAQGRVNAWQAKA 2116
                                           366 EKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQI 414
                                                                                                                          306 NNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNE 365
                                                                                                                                                                                        253 NGCSRSLSFE----PDGQIRASS---SWQSVNESGDQVHWSPGQARLQDQGPSWASGDSS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 MVSGLISDSQITSSNQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,11
REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/115,563
FILING DATE: 02-Apr-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/410,488 FILING DATE: 24-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GLILLAW, JUNGTH S

TITLE OF INVENTION: METHODS FOR DIAGNOSING ACTIVATED PROTEIN

C RESISTANCE ASSOCIATED WITH A FACTOR V GENETIC MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
NNNK--QWLEIDLLKIKKITAIITQGCKSLSSEMYVKSYTIHYSEQGVEWKPYRLKSSMV 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 10666 NO. US20030008307Alth Torrey Pines Road, TPC CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: The Scripps Research Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92037
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                                                                                                                                                                                                                                           Score 317; DB 9;
Pred. No. 2.2e-15;
30; Mismatches 52
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                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                   Length 2224;
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: SEQ ID NO 2

: LENGTH: 343

: TYPE: PRT

: ORGANISM: Human

US-10-190-593-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity 40.5
Matches 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10190593 Publication No. US20030022221A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/190,593
CURRENT FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, TITLE OF INVENTION: UCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CL001246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LANGIT, Emanual et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1325 - PKEWLQVDFRKTMKVTGITTQGVKSLLISMYVKEFLISSSQDGHNWTLF--LQNGKVKV 1381
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                                                                                                                    304 SSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVN 363
|: :||::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|
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184 NGCANPLGLKNNSIPDKQITASSSYKTWG-----LHLFSWNPSYARLDKQGNFNAWVAGS 238
                                                                                                                                                                                                                                                                                                                                         253 NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVH----WSPGQARLQDQG--PSWASGD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNH 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
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Lynch, Carmel
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40.5%; Pred. No. 7.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Mismatches
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Db 295 GSSKIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC 343
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Search completed: May 15, 2003, 13:21:32 Job time: 31,0681 secs

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Result
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membrane type-ser	membrane-bound	hens	hypothetical prot	coagulation	Ra-reactive factor	complement subcon	paranodir	CRP-ductin-alpha	complement subcon	neurexin IV - mous	complement subcom	procol	protein-tyrosine	intrinsic factor-H	procol

## ALIGNMENTS

coagulation factor V precursor - bovine
C:Species: Bos primigenius taurus (cattle)
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Neuron 7, 295-307, 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: this protein has motifs homologous to complement components CIr C;Comment: This protein is a neuronal cell surface molecule involved in C;Superfamily: Xenopus A5 antigen; CIr/CIs repeat homology; discoidin IC;Superfamily: Xenopus A5 antigen; CIr/CIs repeat homology; discoidin IC;Keywords: duplication; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The A5 antigen, a candidate for the neuronal recognition molecule, A;Reference number: JH0466; MUID:91337458; PMID:1908252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: tadpole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D10467; GB:D01077; NID:g222962; PIDN:BAA01260.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 antigen precursor - African clawed frog
;Species: Xenopus laevis (African clawed frog)
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;363,697,1537/Binding site: sulfate (TYT) (COVALEUL, FRUIT DE PROJECTION 1537/Binding site: Arg-Ser (Coagulation factor Xa) #status predicted;376-377/Cleavage site: Arg-Gly (Protein C) #status predicted;533-534/Cleavage site: Arg-Gly (Protein C) #status predicted;607-688,1712-1738,1894-2048,2053-2208/Disulfide bonds: #status predicted;741-742/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status predicted;741-742/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status predicted;741-742/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin)
                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                   430-584/Domain: discoidin
                                                                                                                                                                                                                                                                                                                                                                                                                                         1-21/Domain: signal sequence #status predicted <SI 22-927/Product: A5 antigen #status predicted <A5A>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 1-927 <TAK>
                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                           27-138/Domain: Clr/Cls repeat homology <ClR1>
147-262/Domain: Clr/Cls repeat homology <ClR2>
274-424/Domain: discoidin I amino-terminal homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: JH0466; JQ0948
                                                                                                                                                                                                                                                                                                           646-812/Domain: MAM homology <MAM>
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                                                                                                                                                                                                                                                        ,261,300,523,844/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
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KRLILRLG-DLDIESQTCASDYLLF---
                                                                                                  LLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSFKKSWWG-----NYWEPFLARLNAQGRVNAWQAKANNNN----QWLQIDLLKIKK 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASHYLKTEY-SKFCPA-----GCRDVAGDISGNMV--DGYRDTSLLCKAAIHAGIIADE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIR 268
                                                  LLSCCCWLLCSLRSSWASRNDKCGDTIKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITAIVTQGCKSLSSEMYVKSYTIHYSDQGTDWKPYREKSSMVDKIFEGNNNVRGHVKNFF 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RYIRISPTGSYNKPALRLELQGC-EVNGCSTPLGMESGKIENKQIT 2070
                                                                                                                                                        112;
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                                                                                                                                                                                Similarity
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                                                                                                                                                        Conservative
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                                                                                                                                                                           8.8%;
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Arg-Ser (thrombin) #status experimental
                                                                                                                                                                                                                                                                                                                                 I amino-terminal homology
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                                                                                                                                                   Score 330; DB 1;
Pred. No. 2.4e-15;
4; Mismatches 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 331; DB 1;
Pred. No. 7.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mochii, M.; Eguchi, G.; Fujisawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
TSSSDQYGPYCGSMTVPKELLLNTSEVTVRF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414
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                                                                                                                                                                                                   Length 927
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                                                                                                                                                                                                                                                                                                                                      <DN2>
                                                                                                                                                        Indels 106;
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Proc. Natl. Acad. Sci. U.S.A. 84, 4846-4850, 1987

A;Title: Complete cDNA and derived amino acid sequence of human factor V. A; Reference number: A28028; MUID:87260886; PMID:3110773

A;A;Accession: A28028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Cripe, L.D.; Moore, K.D.; Kane, W.H.
Biochemistry 31, 3777-3785, 1992
A;Title: Structure of the gene for human coagulation factor V.
A;Reference number: A42344; MUID:92232668; PMID:1567832
A;Accession: A56172
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  A; Residues:
A; Cross-ref
                                                                                                                Proc. Natl. Acad. Sci. U.S. A; Title: Cloning of a cDNA.
                                                                                                                                                       A;Cross-references: GB:M17785
A;Note: parts of this sequence were determined by protein R;Kane, W.H.; Davie, E.W.
                                                                                                                                                                                                                                                                                                   A; Note: parts of this sequence, including the amino end of t R; Rane, W.H.; Ichinose, A.; Hagen, F.S.; Davie, E.W. Biochemistry 26, 6508-6514, 1987
A; Title: Cloning of cDNAs coding for the heavy chain region A; Reference number: A27498; MUID:88107560; PMID:2827731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 48-56;79-89;120-130;191-201;239-249;313-323;368-378;428-437;461-471;533-5
2070;2111-2120;2172-2181 <CR2>
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A; Accession: A42344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coagulation factor V precursor [validated] -
                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1284,'I',1286-1600 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-857,'R',859-864,'R',866-924,'E',926-1763,'I',1765-2212,'T',2214-2224
A;Cross-references: GB:M16967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-2224 <CRI>
                                                                                        A; Reference number: A25897;
                                                                                                                                                                                                                                                                                    A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man);Date: 19-May-1989 #text_change;Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A56172; A42344; A28028; A27498; A25897
                                                                      Accession:
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ī188-1215,1315-2224 <KA2>
erences: GB:M14335
                                                                      A25897
                                                                                                                                                                                                                                                                                    A27498
                                                mRNA
                                                                                                                   U.S.A. 83, 6800-6804, 1986
DNA coding for human facto
                                                                                          MUID:86313665;
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                                                                                                                   factor
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homo

plasm

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F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-224/Product: coagulation factor V #status predicted <MAT:
F;29-31/Product: coagulation factor Va heavy chain #status ex
F;29-345/Domain: Al CDAl>
F;33-329/Domain: Al CDAl>
F;33-329/Domain: Az CDA2>
F;351-684/Domain: Az CDA2>
F;351-684/Domain: B <DOB2>
F;1613/Domain: B <DOB2>
F;162-1573/Domain: B <DOB3>
F;1613-1461/Region: 9-residue repeats (Q-X-T/N-L-S-P-D-L-S)
F;1574-2224/Product: coagulation factor Va light chain #status
F;1657-1765/Region: presidue repeats (Q-X-T/N-L-S-P-D-L-S)
F;1651-1905/Domain: A3 <DA3>
F;1651-1765/Region: phospholipid binding #status predicted
F;1906-2064/Domain: C1 <DC1>
                                                                                                                                                                                                       coagulation factor V - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revisio
                                                                                                                                                                                                                                                                                                                       RESULT
T42764
                                                                                                     C; Accession: T42764
R; Yang, T.L.; Cui, J.; Re
Blood 91, 4593-4599, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 53/2;
C; Function:
A; Description: a
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       A;Title: The structure and function of murine factor V and A;Reference number: 222270; MUID:98282202; PMID:9616155 A;Accession: T42764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1573-1574/Cleavage site: Arg-Ser (thrombin) #status experimental
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Best Local S
Matches 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Gene: GDB:F5
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Thomain: signal sequence #status predicted <SIG>
24/Product: coagulation factor V #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKIFEGNTNTKGHVKNFFNPPIISRFIRVIPKTWNQSIALRLELFGCDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQI
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1q23-1q23
84/1; 125/1; 196/1; 244/1;
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                                                                                                                                                                                                              #sequence_revision
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                                                                                                                                             Rehumtulla,
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42.6%;
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Pred. No. 3.
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ags protein precursor - rat
N;Alternate names: O-acetyl-Gd3 ganglioside
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Sep-1996 #sequence_revision 01-Nc
C;Accession: JC4915.
R;Ogura, K; Nara, K; Watanabe, Y; Kohno,
Biochem. Biophys. Res. Commun. 225, 932-938,
                                                                                                                                                                                                                                       RESULT
JC4915
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A; Molecule type: mRNA
A; Residues: 1-2183 < YAN>
A; Residues: 1-2183 < YAN>
A; Cross references: EMBL: U52925; N:
C; Function: C; Function
A; Pathway: blood coagulation factor V
C; Superfamily: coagulation; dupl
C; Keywords: blood coagulation; dupl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            milk fat globule protein - human (fragm
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision
C;Accession: A47285
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A; Residues: 1-218 < LAR>
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A;Title: A M-r 46,000 human
A;Reference number: A47285;
A;Accession: A47285
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                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                   Cross-references: GB:S56151; NID:9235396; PIDN:AAB19771.1; PID:9235397; Superfamily: milk fat globule protein; discoldin I amino-terminal homoly: J-56/Domain: discoldin I amino-terminal homology (fragment) <DN1>;60-218/Domain: discoldin I amino-terminal homology <DN2>
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Best Local :
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170 GSSKIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC
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                                 NEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC
                                                                                               SSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNENFYVKSFVMNFKNNNSKWKTYKGIVN 363
                                                                                                                                                  NGCANPLGLKNNSIPDKQITASSSYKTWG-----LHLFSWNPSYARLDKQGNFNAWVAGS
                                                                                                                                                                                       NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVH---WSPGQARLQDQG--PSWASGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGCSTPLGLEDGRIQDKQITASSFKKSWW-----GD--YWEPSLARLNAQGRVNAWQAKA
                                                                                                                                                                                                                            63;
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                                                                                                                                                                                                                                                Similarity
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                                                                          -QWLQVDLGSSKEVTGIITQGARNFGSVQFVASYKVAYSNDSANWTEYQDPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.A.; Urrea, R.; Kuniyoshi,
8, 1991
                                                                                                                                                                                                                                              7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     milk fat globule protein that MUID:91371351; PMID:1909932
                                                                                                                                                                                                                            33;
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                                                                                                                                                                                                                         Score 299; DB
Pred. No. 4.5e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID: g3219690;
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Pred. No. 6.2e-14;
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                                                                                                                                                                                                                                                DB 2;
.5e-14;
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                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                          Gaps
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rat) on 01-Nov-1996

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A; Reference number: A44258;
A; Accession: A44258
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision
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F;110-267/Domain: discoidin I amino-terminal homology
F;271-427/Domain: discoidin I amino-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: CST cell C; Comment: This protein is required
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                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-216 <LEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor VIII-associated gene B hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-427 <OGU>
                                                                                                                                                    Superfamily: coagulation factor VIII; discoidin I amino-terminal h;1-53/Domain: discoidin I amino-terminal homology #status atypical;57-210/Domain: discoidin I amino-terminal homology <DN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF;1-21/Domain: signal sequence #status predicted <SIG>;28-60/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                 Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: DDBJ:D84068; NID:g1620006; PIDN:BAA12210.1; Experimental source: CST cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                               Matches
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                                      NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGTSKVFQGNLDNNSHKKNIFEKPFMARYVRVLPLSWHNRITLRLELLGC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDKRFLFTS--
  NSCSMPLGMESKAISDAQITASSYFTNMFAT - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIV:::::|||:|||:||||||:::::|||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCELHGCSEPLGLKNNTIPDSQITASSSYKTWNLRA--FGWYPHLGRLDNQGKINAW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGRRFEFIQDESGTGDKEFMGNQDNNSLKINMFNPTLEAQYIRLYPVSCHRGCTLRFELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARLYRTGIVNAWTASSYDSKPWIQVDFLRKMRVSGVMTQGA-SRAGRAEYLKTFKVAYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVLQRKGI-----SL 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TAQSNSAKEWLQVDLGTQKKVTGIITQGARDFGHIQYVASYKVAHSDDGVQWTVYE--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGP--SWASG 302
                                                                             . Similarity
62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                               7.6%;
37.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                           Score 285.5; DB 2;
Pred. No. 4.2e-13;
2; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                                                          P.; Fisher, K.; Gitschier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 30-Sep-1993 #text_change
  WSPSKARLHLQGRSNAWRPQVNN-
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167
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                                                                                        KPREWLEIDLGEKKKITGIRTTGSTQSNENFYVKSFVMNFKNNNSKWKTYKGIVNNEEKV
                                                                    -PKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLF--FQNGKVKV 166
                             FQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQ 413
FQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCE
211
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coagulation factor VIII precursor [validated] - human N;Alternate names: antihemophilic factor A; coagulation coagulation factor VIIIc; procoagulant co

C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 \*sequence\_revision
C;Accession: I54318; A00525; I58059; A R; Gitschier, J.; Wood, on 28-Aug-1985 #text\_change 08-Dec-2000 A23584; A26174; A42348; A43986; S63527; S66445;

Hum. Mol. Genet. 1, 199-200, 1992 A;Title: Sequence of the exon-containing regions of the A;Reference number: I54318; MUID:93265012; PMID:1303178 A;Accession: I54318 human factor VIII

gene

A; Molecule type: DNA A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1 1921,'S', 1923-2351 <RES>
A;Cross references: GB.M88648; NID:g182381; PIDN:AAA52420.1; PID:g182383; PIV:WOOD, WI.; Capon, D.J.; Simonsen, C.C.; Eaton, D.L.; Gitschler, J.; Kinature 312, 330-337, 1984

A;Title: Expression of active human factor VIII from recombinant A;Reference number: A00525; MUID:85061548; PMID:6438526 A;Accession: A00525 DNA clones

A; Molecule type: mRNA A; Residues: 1-2351 <WOO>

R;Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pis, D.N.; Hewick, R.M.
Nature 312, 342-347, 1984
A;Title: Molecular cloning of a cDNA encoding human antihaemophilic factor.
A;Reference number: I58059; MUID:85061550; PMID:6438528 A;Cross-references: EMBL:X01165; EMBL:X01166; EMBL:X01179 R;Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, Þ

A; Accession: I58059 Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-74,'V','6-1259,'E',1261-2351 <RE2>
A;Residues: 1-74,'V','6-1259,'E',1261-2351 <RE2>
A;Cross-references: GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g182803
A;Cross-references: GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g182803
A;Cross-references: GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g182803
A;Cross-references: GB:K01740; NID:g182803
A;Cross-references: GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g182803
A;Cross-references: GB:K01740; NID:g182803
A;Cross-references: GB:K01740; Hartog, K.;

A; Title: Characterization of the polypeptide composition of human factor VIII:C A; Reference number: A23584; MUID:86081164; PMID:3935400 ٦.;

A; Accession: A23584

A; Molecule type: mRNA A; Residues: 1-2351 <TRU>

PID:g182818

A;Cross-references: GB:M14113; NID:g182817; PIDN:AAA52485.1; R;Eaton, D.; Rodriguez, H.; Vehar, G.A.
Biochemistry 25, 505-512, 1986 A; Title: Proteolytic processing of human factor VIII. Correlation of specific

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A; Accession: A; Reference number: A26174; A26174 MUID:86159740; PMID:3082357

A; Molecule type: protein A; Molecule type: protein A; Residues: 20-36;392-399, 'X', 401-402;1668-1678;1709-1722, 'D',1723-1725;1741-1755 R; Pittman, D.D., Wang, J.H.; Kaufman, R.J. Biochemistry 31, 3315-3325, 1992 Biochemistry 31, 3315-3325, 1992 A; Fittle: Identification and functional importance of tyrosine sulfate residues with A; Reference number: A42348; MUID:92207952; PMID:1554716 A; Recession: A42348

residues within

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A; Note: Sugardain, T.M.
R; Fay, P.J.; Smudzin, T.M.
264, 14005-14010, A;Molecule type: protein
A;Residues: 20-36;356-371;392-408;582-594;1668-1669,'X',1671;1672-1692;1693-1708;1709
A;Residues: 20-36;356-371;392-408;582-594;1668-1669,'X',1671;1672-1692;1693-1708;1709
A;Ryperimental source: recombinant material from Chinese hamster ovary cells
A;Note: sequence extracted from NCBI backbone and corrected to correspond with the pu

fluorescence 1989

energy transfer in human tactor

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A;Gene: GDB:F8C
A;Cross-references: C
A;Map position: Yq28
A;Introns: 48/2; 89/1
C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Locations of disulfide bonds and free cysteines in A;Reference number: A56216; MUID:95338127; PMID:7613471 A;Reference number: A56216; MUID:95338127; PMID:7613471 A;Ronten: 329-Cys, 711-Cys, and 2019-Cys were shown to have in R;Kjalke, M.; Heding, A.; Talbo, G.; Persson, E.; Thomsen, Eur. J. Blochem. 234, 773-779, 1995
A;Title: Amino acid residues 721-729 are required for full A;Reference number: S63527; MUID:96163459; PMID:8575434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: protein
A;Residues: 1668-1685 <L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction A;Reference number: S66445; MUID:96048024; PMID:7556150
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A; Title: Sulfation of
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#status
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Ezban, M.
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A; Molecule type: mRNA
A; Residues: 1-463 <STU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Keywords: membrane protein
F:28-60/Domain: EGF homology <EG1>
F:68-107/Domain: EGF homology <EG2>
F:147-303/Domain: discoidin I amino-terminal
F:307-463/Domain: discoidin I amino-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               milk fat globule membrane protein - mouse C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A36479
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                                                                                                                                                               234 KTFKVAYSLDGRKFEFIQDESGGDKEFLGNLDNNSLKVNMFNPTLEAQYIRLYPVSCHRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 CASDYLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGR------
                                KINAW----TAQSNSAKEWLQVDLGTQRQVTGIITQGARDFGHIQYVESYKVAHSDDGVQ
WKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC
                                                                 P--SWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSK 354
                                                                                                 CTLRFELLGCELHGCLEPLGLKNNTIPDSQMSASSSYKTWNLRA---FGWYPHLGRLDNQG
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112; Conserv
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                                                                                                                              ----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQG
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Pred. No. 5.8e
59; Mismatches
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Pred. No. 1.
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A; Residues: 1-2133 <LOL>
A; Cross-references: EMBL: U49517; NID: g1511633; PID: g1511634; PIDN: AAB06705.1
C; Superfamily: coagulation factor VIII; discoldin I amino-terminal homology; C; Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemople
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R;Elder, B.; Lakich, D.;
Genomics 16, 374-379, 199
A;Title: Sequence of the
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                                                                                                                                                                                                      F;23-349/Domain: ferroxidase repeat homology <FOX1>
F;402-730/Domain: ferroxidase repeat homology <FOX2>
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                                                                                                                                                                                                                                                    F;20-2133/Product:
                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;402-730/Domain: ferroxidase repeat homology <FO2>F;1686-2006/Domain: ferroxidase repeat homology <FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-2319 <ELD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A47004; A; Accession: A47004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L05573; NID:g192456; PIDN:AAA37385.1; PID:g192457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                              ;1498-1820/Domain: ferroxidase repeat homology <FOX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Sus scrofa
;Date: 11-Jan-2000 #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;1686-2006/Domain: ferroxidase repeat homology <FO3>;2007-2156/Domain: discoidin I amino-terminal homology;2160-2313/Domain: discoidin I amino-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: coagulation factor VIII; discoidin I amino-terminal; 1-19/Domain: signal sequence #status predicted <SIG>; 2-349/Domain: ferroxidase repeat homology <FO1>
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                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: T42763
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Best Local
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                                                                                                                                                                                                                                                1-19/Domain: signal sequence #status predicted <SIG>
20-2133/Product: coagulation factor VIII #status predicted
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                                            253 NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNH 308
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                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PKQWLQVDLQKTMKVTGIITQGVKSLFTSMFVKEFLISSSQDGHHWTQI--LYNGKVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSCSIPLGMESKVISDTQITASSYFTNMFAT----WSPSQARLHLQGRTNAWRPQVND-
  NSCSMPLGMQNKAISDSQITASSHLSNIFAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQGNQDSSTPMMNSLDPPLLTRYLRIHPQIWEHQIALRLEILGCEAQQ 2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor VIII precursor - pig
us scrofa domestica (domestic pig)
an-2000 #sequence_revision 11-Jan-2000
                                                                                          Conservative
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04; MUID:93300511; 1
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                                                                                   Score 271.5; DB 2;
Pred. No. 1.3e-10;
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WSPSQARLHLQG-----RTNAW 2020
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                                                                                                                                  Length
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                                                                                                                                    2133;
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C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
C;Accession: S74211; S78114; S24181
                                           A; Reference number: A; Accession: S74211
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                                                                                    Eur. J. Biochem. 240, 628-636, 1996
A; Title: Characterization of glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: glycoprotein
F; 1-32/Domain: EGF homology (fragment) <EG1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A48394; MUID: 93250576; PMID: 8485470 A; Accession: G48394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: glycoprotein component 16/major C; Species: Bos primigenius taurus (cattle) C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997
A; Molecule type: mRNA
A; Residues: 1-427 <HVA>
                                                                                                                                R; Hvarregaard, J.; Andersen, M.H.; Berglund,
                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: sequence extracted from NCBI backbone (NCBIP:131457) C; Superfamily: milk fat globule protein; discoidin I amino-tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title:
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40-79/Domain: EUE homology <EG2>
82-239/Domain: discoidin I amino-terminal homology <DN1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGCTEPLGLKDNTIPNKQITASSYYKTWGLSA--FSWFPYYARLDNQGKFNAWTAQTNSA 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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iol. Int.
                                                                                                      240, 628-636, 1996
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                                                                  S74211; MUID:97008954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L.R.; Lane, W.S.
29, 545-554, 1993
                                                                                                                                                                                                                         bovine
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                                                                                      PAS-6/7
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                                                                  PMID:8856064
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                                                                                      bovine milk fat
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EMBL: X91895;

NID:g1632778; PIDN:CAA62997.1; PID:g1632779

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A;Accession: 5,611.
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 19-85;96-110;140-165;174-216;221
A;Residues: 19-85;96-110;140-165;174-216;221
R;Kim, D.H.; Kanno, C.; Mizokami, Y.
Blochim. Blophys. Acta 1122, 203-211, 1992
A;Title: Purification and characterization
. n-farance number: S23926; MUID:92353107;
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                                                                                                                                                                                                                                                                                              A;Description: may be involved in membrane remodeling and/or function C;Superfamily: unassigned EGF-related proteins; EGF homology F;6-40/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Y116
A;Experimental source: testis
C;Function:
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A; Title: Molecular cloning and characterization of P47, a A; Reference number: Z17325; MUID:98206817; PMID:9546740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pP47 protein - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T11743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Ensslin, M.; Vogel
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F;108-265/Domain: discoidin I amino-terminal homology <DN1>
F;269-427/Domain: discoidin I amino-terminal homology <DN2>
F;269-427/Domain: discoidin I amino-terminal homology <DN2>
F;24-35,29-47,49-58,66-77,71-94,96-105/Disulfide bonds: #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: milk fat globule protein; discoidin I amino-terminal homology; C;Keywords: blocked amino-end; disulfide bond; glycoprotein; milk F;I-18/Domain: signal sequence #status predicted <SIG>F;19-427/Product: PAS-6/7 protein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-409 <EN
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Matches 61
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Residues: 19-85;96-110;140-165;174-216;221-232;248-277;285-293;309-337;339-420;425-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         slin, M.; Vogel, T.; Calvete, J.J.; Thole, H.H.; Schmidtke, Reprod. 58, 1057-1064, 1998
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                                                                                                 72
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AGIVNAWTASNYDRNPWIQVNLLRR--
                                                                                               TEYICKCPHGYTGIHCEIICNAPLGMETGAIADFQISASSMHLGFMGLQRWAPELARLHR
                                                                                                                                             TEYSKFCPAGCRDVAGDISGNMVDGYRDTSL----LCKAAIHAGII-----ADELGG---
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Similarity 36.7%;
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                                                                                                                                                                                              6.9%; Score 259.5; DB 2; ilarity 25.0%; Pred. No. 7.9e-11; Conservative 46; Mismatches 102;
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0; Mismatches
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Pred. No. 2.1e-11;
-MRVTGVVTQGA-SRAGSAEYMKTFKVAYSTDG
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A;Residues: 1-845 <OHN>
A;Cross-references: DDBJ:D86479; NID:g1468942; PIDN:BAA13094.1; PID:g1468943
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C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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RQLMKVVNEECPTITRTYSLGKSSRGLKIYAMEI
                                                      RFTGVITQGRDSSIHDDFVTTFFVGFSNDSQTWVMYTN--GYEEMTFHGNVDKDTPVLSE
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                            QSTSVSTKKEDETITRPIPSEETSTGINITTVAI
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1: /cgn2_6/ptodata/1.

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Gapop 10.0 , Gapext 0.5
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Query Match 9.6%; Score 360.5; DB 4; Best Local Similarity 22.5%; Pred. No. 7.4e-23; Matches 144; Conservative 99; Mismatches 246;	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/116,473 FILING DATE: 17-JUL-1998 CLASSIFICATION: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 60/052,762 FILING DATE: 17-JUL-1998 ATTORNEY/ACENT INFORMATION: NAME: Kagan, Sarah A REGISTRATION NUMBER: 32141 REFERENCE/DOCKET NUMBER: 01107.74973 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100 TELEFAX: 202-508-9299 TELEX: SEQUENCE CHARACTERISTICS: LENGTH: 925 amino acids TYPE: amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear US-09-116-473-2	RESULT 1 US-09-116-473-2 Sequence 2. Application US/0911647 Sequence 2. Application US/0911647 Sequence 2. Application US/0911647 Sequence 2. Application US/0911647 Particle Of INFORMATION: APPLICANT: Kolodkin, Alex APPLICANT: Kolodkin, Alex APPLICANT: Kolodkin, Alex APPLICANT: Ginty, David TITLE OF INFORMATION: SEMAPHORIN NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: Banner & Witcoff STREET: 1001 G Street, NW STATE: DC COMPITEY: Washington STATE: DC COMPITEY: USA ZIP: 20001 COMPUTER: LOSS MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: TISK COSS OPERATING SYSTEM: DOSS	28 285.5 7.6 1661 2 US-08-882-083-2 29 285.5 7.6 1661 2 US-08-58-107-2 30 285.5 7.6 1661 4 US-09-243-539-2 31 285.5 7.6 2332 1 US-07-864-0048-4 32 285.5 7.6 2332 1 US-08-251-937A-4 33 285.5 7.6 2332 1 US-08-276-594A-2 34 285.5 7.6 2332 1 US-08-76-594A-2 35 285.5 7.6 2332 1 US-08-76-7077A-2 36 285.5 7.6 2332 1 US-09-037-601-2 37 285.5 7.6 2332 4 US-09-037-601-2 38 285.5 7.6 2332 4 US-09-315-179-2 40 285.5 7.6 2332 4 US-09-315-179-2 41 285.5 7.6 2332 4 US-09-523-656-2 42 285.5 7.6 2332 5 PCT-US93-03275-4 43 285.5 7.6 2351 1 US-08-121-202-2 44 285.5 7.6 2351 1 US-08-121-202-2 45 285.5 7.6 2351 6 5171844-2
Length 925; Indels 151; Gaps 25;			Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

41 CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 98

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US-08-936-135-22
; Sequence 22, Application US/08936135
; Patent No. 6054293
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                          ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tessier-Lav
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CALIFORN—CONTROL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534
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                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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REFERENCE/DOCKET
                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                             APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLITSDMADYQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPRNPQAQPGEEW-LQVDLGTPKTVKGVIIQGARGGDSITAMEARAFVRKFKVSYSLNGK 533
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NUMBER:
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UC97-288-2
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RESULT 3 US-08-936-135-24

Sequence 24, Application Patent No. 6054293 GENERAL INFORMATION:

US/08936135

APPLICANT: Tessier-I
APPLICANT: He, Zhiga
APPLICANT: Chen, Hau
TITTLE OF INVENTION:

Chen, Hang He, Zhigang

Tessier-Lavigne,

Marc

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE:

SCIENCE & TECHNOLOGY LAW GROUP

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TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 901 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650) 343-4341
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577
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                    AARLVSSRSGWFPRNPQAQPGEEW-LQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVR 522
                                                                                                                                                                                                                                       ARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRPI 445
                                                                                                                                                                                                                                                                                                                                                                             SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SD--
RWSPAGIGMRLEVLGCDWTDSKPTVETLGPTVKSEETTTPYPMDEDATECG
                                                                                                                                                                                                      TRFTRTRPQTWHLGTALRLELFGCRVTDAPCSNMLGMLSGLTADTQTSASSTREYLWSPS
                                                                                                                                                                                                                                                                           GAISRETQKGYYVKSYKLEVSTNGEDWMYYRHGKNH--KIFQANNDATEVVLNKLHMPLL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS 149
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                              --NEKEMTQKLDLITSDMADYQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPRMEIILQFLTFDLEHDPLQVGEG
                                                                 KFKVSYSLNGKD-----WEYIQDPRTQQTKLFEGNMHYDTPDIRRFDPVPAQYVRVYPE
                                                                                                 KKKKGSPYGSAEAQKTDCWKQIKYPFARHQSA-EFTISYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                   IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------EGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFEPDGQIRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRY-- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEIRDGDSESADLLGKHCGNI-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140;
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                                                                                                                                                                                                                                                                                                                                            ---WTPQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQ 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%; Score 354.5; DB 3
21.5%; Pred. No. 2.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---HPDLITC----LERASHYLKTEYSKF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
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INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
TYPE: amino acid
STRANDEDWESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-936-135-24
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Best Local Similarity 21.5%;
Matches 140; Conservative 9
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NAME: OSMAN, RICHARD A
REGISTRATION UNUBER: 36,627
REFERENCE/DOCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343,4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                346
                                                                                                                                   446
                                                                                                                                                                                                                                                                                      331 G--STQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDFVQNNFIPPIV 388
      523
                                                                                                                                                                                                  389 ARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRPI 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPRMEIILQFLTFDLEHDPLQVGEG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 SD------ 173
                                           483 KKKKGSPYGSAEAQKTDCWKQIKYPFARHQSA-EFTISYD------------
                                                                                   464 AARLVSSRSGWEPRNPQAQPGEEW-LQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVR 522
                                                                                                                                                                          404 TRFIRIRPOTWHLGIALRLELFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSPS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 DCKYDWLDIWDGIPHYGPLIGKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 IEIRDGDSESADLLGKHCGNI-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 CGGRPNSKDAGYITSPGYPQDYPSHQNCEWIYYAPEPNQKIVLNFNPHFEIEKHDCKYDF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                           GAISRETQKGYYVKSYKLEVSTNGEDWMYYRHGKNH--KIFQANNDATEVVLNKLHMPLL 403
                                                                                                                                                                                                                                                                                                                                                                                            SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT 330
KFKVSYSLNGKD-----WEYIQDPRTQQTKLFEGNMHYDTPDIRRFDPVPAQYVRVYPE 576
                                                                                                                                                                                                                                                                                                                                                                                                                                       IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR-------
                                                                                                                                                                                                                                                                                                                                                 --WTPQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFEPDGQIRAS 270
                                                                                                                              ---PSEETSTGINITTVAIPLVLLVVLVFAGMGIFA----AFRK 482
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Pred. No. 2.4e-22;
96; Mismatches 242; Indels 173; Gaps
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2	1 CGMOCVNECCDOVINGECOADIODOCEANOCODECUNIUS DE SUI STOLOSSES TOTO I SERVITORO	7 271	2
30	7 IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR	267	탕
27	9SGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFEPDGQIRAS	/ 229	γΩ
26	4 "CPAGCKDYAGDIS" GNMYDGIKTISLIKKAAIHAGIIADELGGQISYLQKKGISKI"   	0 207	B 6
	EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPRMEIILQFLTFDLEHDPLQVGE	_	P 5
17	O SDRPDITTCIERASHYIKTEVSKE	, 150	Ş
14		88	밁
14	LLFTSSSDQYGPYCGSMTVPKELLLNTSEVTV	, 99	Qγ
87			밁
98	CGHLVTYQDSGTM	/ 41	Qγ
Gaps	atch 9.4%; Score 354.5; DB 3; Length 909; cal Similarity 21.5%; Pred. No. 2.4e-22; Indels 173; 140; Conservative 96; Mismatches 242; Indels 173;	Query M Best Lo Matches	
	PE	6-80- OM	ös ;
	STRANDEDNESS: single TOPOLOGY: linear	H W	
	TYPE: amino acid	нг	
	EQUENCE CHARACTERISTICS:	SEQ	
	TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO: 8:	INFOR	٠. ٠.
	TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 343-4341	13.1	<b></b> .
	NUMBER:		٠
	NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36,627	# Z	
	TORNEY/AGENT INFORMATION:	, ATT	٠. ٠.
	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936.135	COR	
	ARE: PatentIn Release	5 00 0	٠
		20	
	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	. Y	
	94010	2	
	STATE: CALIFORNIA COUNTRY: USA	റ	
	BOROUGH	. O	
	ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP	יב' מ'	
	ONDENCE ADDRESS:	COR	
	R OF IN	NIMBE	
	CANT: Chen, Hang	APP	٠
	APPLICANT: Tessier-Lavigne, Marc	APP	
	INFORM	8	٠
	ce 8, Application US/08936135	Sequence Patent N	<b>-</b> .
	4 36-135-8	RESULT 4	무건
	7 RWSPAGIGMRLEVIGCDWTDSKPTVETLGPTVXSBETTTPVPMDEDATBCG 627	577	문
	2NEKEMTQKLDLITSDMADYQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG 569	7 522	δō

22;

303 270 266 228 206 173 146 149 . 87 98

CGHLVTYQDSGTWTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASI     : :  :	Query Match 9.4%; Score 354.5; DB 3; Length 909; Best Local Similarity 21.5%; Pred. No. 2.4e-22; Matches 140; Conservative 96; Mismatches 242; Indels 173; Gaps	STRANDEDNESS: single TOPOLLOGY: linear MOLECULE TYPE: peptide US-08-936-135-10	SEQUENCE CHARACTERISTICS: LENGTH: 909 amino acids	TREDEPHONE: (650) 343-4341  TELEFAX: (650) 343-4342  TREDEPATION FOR SED ID NO. 10.	REGISTRATION NUM	ATTORNEY PAGENT INFORMATION:	; CURRENT APPLICATION DATA: ; APPLICATION UNMBER: US/08/936,135	COMPUTER READABLE FORM:  KANDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30	CITY: HILLSBURUUGH STATE: CALIFORNIA COUNTRY: USA ZIP: 94010	DENCE ADDRESS SE: SCIENCE 75 DENISE D	; AFFLICANY: TESSIET-LAVIGNE, MAIC; APPLICANY: He, Zhigang; APPLICANT: Chen, Hang; TITLE OF INVENTION: Semaphorin Receptors; NIMPRER OF SEQUENCES: 26	0 Application US/0893 54293 RMATION:	SULT 5	QY 522NEKEMTQKLDLITSDMADYQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG 569  577 RWSPAGIGMRLEVLGCDWTDSKPTVETLGPTVKSSFTFTPVFNFDATEGA 627	Db 523 KFKVSYSLNGKDWEYIQDPRTQQTKLFEGNMHYDTPDIRRFDPVPAQYVRVYPE 576	Oy 483 KKKKGSPYGSAEAQKTDCWKQIKYPFARHQSA-EFTISYD 521	Qy 446PSEETSTGINITTVAIPLVLLVVLVFAGMGIFAAFRK 482	Db 404 TREIRIRPQTWHLGIALRLELEGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLMSPS 463		Qy 331 GSTQSNENEYVKSEVMNEKNNNSKWKTYKGIVNNEEKVEQGNSNERDPVQNNEIPPIV 388	Db 304WTPQQSRLHGDDNGWTPNLDSNKEYLQVDLRFLIMLTAIATQ 345
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NAME: OSMAN, RICHARD A RECISTRATION NUMBER: 36,627 REGISTRATION NUMBER: UC97-288-2 REFERENCE/DOCKET NUMBER: UC97-288-2 TELECOMMUNICATION INFORMATION:	APPLICATION NUMBER: US/08/936,135 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:	MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOTTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:	<u> </u>	SH.	ESPONDI DRESSEI	ICANT: He, Znigar ICANT: Chen, Hang ICANT: Chen, Hang ICANTION: S	CANT: Tes	RESULT 6 US-08-936-135-12 ; Sequence 12, Application US/08936135 ; Patent No. 6054293	Qy 522NEKEMTQKLDLITSDMADYQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG 569 : : :::     : : : : : :	Db 523 KFKVSYSLNGKDWEYIQDPRTQQTKLFEGNMHYDTPDIRRFDPVPAQYVRVYPE 576	446	ARYVRVVPQTWHQRIALK  :: :         : TRFIRIRPQTWHLGIALR	Db 346 GAISRETQKGYYVKSYKLEVSTNGEDWMYYRHGKNHKIFQANNDATEVVLNKLHMPLL 403	304WTPOQSRLHGDDNGWTPNLDSNKEYLQVDLRFLTMLTALATQ	Qy 271 SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT 330	267 IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR	Db 207 DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYL 266  Qy 229EGILANGYLSRDGSLSDKRFLFTSNGCSRSLSFEDDGOTRA'S 270.		147 EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPRMEIILQFLTFDLEHDPLQVGEG	Db 88 IEIRDGDSESADLLGKHCGNI-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGS 146	QY 99 LLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYAS 149

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GENERAL INFORMATION:
APPLICANT: Tessier Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
ITILE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
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US-08-936-135-14
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                                                                                                                                                             Sequence 14, Application US/08936135 Patent No. 6054293
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Best Local Similarity 21.5%;
Matches 140; Conservative 9
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TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                               --NEKEMTQKLDLITSDMADYQQPL-MIGTGTVTRKGSTFRPMDTDAEEAG 569
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Pred. No. 2.5e-22;
6; Mismatches 242;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135
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                                    483 KKKKGSPYGSAEAQKTDCWKQIKYPFARHQSA-EFTISYD------
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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ZIP: 94010
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        KFKVSYSLNGKD-----WEYIQDPRTQQTKLFEGNMHYDTPDIRRFDPVPAQYVRVYPE 576
                                                                    AARLVSSRSGWFPRNPQAQPGEEW-LQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVR
                                                                                                                                  TRFIRIRPQTWHLGIALRLELFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSPS
                                                                                                                                                    ARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRPI 445
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Pred. No. 2.5e-22;
6; Mismatches 242;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                            147
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                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT 330
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                                            IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR-------
                                                                                                 DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYL 266
                                                                                                                             -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRY--
                                                                                                                                                         EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPRMEIILQFLTFDLEHDPLQVGEG 206
                                                                                                                                                                                                                IEIRDGDSESADLLGKHCGNI-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGS 146
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                                                                                                                                                                                                                                            LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS 149
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSMAN, RICHARD A
OSMAN, WIMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94010
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                                                                     -----EGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFEPDGQIRAS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343-4342
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                                                                                                                                                                                     ----HPDLITC----LERASHYLKTEYSKF-------
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                                                                                                                                                                                                                                                                                                                                            Score 354.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                             2.5e-22;
                                                                                                                                                                                                                                                                                                                                                         DB 3;
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Patent No.
                                                                                                 Query Match
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APPLICANT: Tessie:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650) 343-434
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
NAME: OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 AARLVSSRSGWFPRNPQAQPGEEW-LQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 G--STOSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFOGNSNFRDPVQNNFIPPIV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: /J LL...
CITY: HILLSBOROUGH TOORNIA
                                             41 CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 98
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF
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                                                                                                                                                                                                  h 9.3%; Score 351.5; DB 3; Similarity 22.2%; Pred. No. 4.5e-22;
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                   Length 909;
                                                                                                                                                             Indels 143;
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Gaps

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US-08-936-135-20
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Patent No. 6054293
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC97-288-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               ZIP: 94010
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Semaphorin Receptors NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 CLASSIFICATION: 435
                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WTD-SKPTVKTLGPTVKSEETTTPYPTEEE----ATECG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CWKQIKYPFARHQSA-EFTISYD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAQPGEEWLQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVRKFKVSYSLNGKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP------IP
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                                                                                                                                                Patent No. 6054293
GENERAL INFORMATION:
APPLICANT: Tessie
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                                                  TITLE OF INVENTION: SE NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acid
                                                                                                             APPLICANT:
                                                                                                                                APPLICANT:
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STRANDEDNESS: sir
TOPOLOGY: linear
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                 STREET:
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                                                                                                                                                                                                                                                                                                  WTD-SKPTVKTLGPTVKSEETTTPYPTEEE---
                                                                                                                                                                                                                                                                                                                                     MADYQQPLMIGTGTVTRKGSTFRPMDTDAEEAGVSTDAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
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                                                                                                                                                                                   , Application US/08936135 6054293
 HILLSBOROUGH
               75 DENISE DRIVE
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                                                                        Chen, Hang
VENTION: Semaphorin Receptors
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He, Zhigang
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Pred. No. 4.6e-22;
9; Mismatches 255;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-936-135-6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/936,135
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: US/08/936,135
FILECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.0%; Score 338.5; DB 3; Length 923; Best Local Similarity 20.8%; Pred. No. 6.5e-21; Matches 158; Conservative 106; Mismatches 267; Indels 227; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
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LENGTH: 923 amino acids
TYPE: amino acid
523 EKEMTQKLDLITSDMADYQQPLMIGTGTVTRKGSTFRPMDTDAEEAGVSTDAGGHYDCPQ 582
                                                    475 -----PSPHPY-----TNEWLQVDLGDEKIVRGVIIQGGKHRENKVFMRKFKIAYSN 521
                                                                                                  479 AFRKKKKKGSPYGSAEAQKTDCWKQI-------KYPFARHQSAEFTISYDN 522
                                                                                                                                                            431 CSGMLGMVSGLISDSQITASNQADRNWMPENIRLVTSRTGWALP------
                                                                                                                                                                                                          425 KTSQSTSVSTKKEDETITRPIPSEETSTGINITTV-----AIPLVLLVVLVFAGMGIFA 478
                                                                                                                                                                                                                                                               377 KAIIFQGNTNPTDVVLGVFSKPLITRFVRIKPVSWETGISMRFEVYGCKITD-----YP 430
                                                                                                                                                                                                                                                                                             365 EEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWR 424 : :||||:| | | | ::: |: ||:|| : :
                                                                                                                                                                                                                                                                                                                                                                    323 ----KEWIQVDLGLLREVTAVGTQGAISKETKKKYYVKTYRVDISSNGEDWISLK--EGN 376
                                                                                                                                                                                                                                                                                                                                                                                                  307 NHKPREWLEIDLGEKKKITGIRTTG--STOSNFNFYVKSFVMNFKNNNSKWKTYKGIVNN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 ----CMEALGMESGETHSDQITASSQYGT-----NWSVERSRLNYPENGWTPGEDSY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 IGRYCGQKTPGRIRSSSGVLSMVFYTDSAIAKEGFSANYSVLQSSI-SEDFK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 -----LERASHYLKTEYSKFCPAG--CRDVAGDISGNMVDGYRDTSLLCKAAIH 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 GPFLFIKFVSDYETHGAGFSIRYEIFKRGPECSQNYTAPTGVIKSPGFPEKYPNCLECTY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 TSNGCSRSLSFEP----DGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 TITVPKG-KRLILRLG-DLDIESQTCASDYLLFTSSSDQ----YGPYCGSMTVPKELLLN 124
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'Qy 159LERASHYLKTEYSKFCPAGCRD	Qy 125 TSEVTVRFESGSHISGRGFLLTYA : ::          :   Db 116 GPFLFIKFVSDYETHGAGFSIRYEIFKRGPECSQN	Qy 71 TITVPKG-KRLILRLG-DLDIESQTCASDYLLFTSSSDQYGPYCGSMT	Oy 17 RGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEK	Query Match  8.8%; Score 331;  Best Local Similarity 24.1%; Pred. No. 3  Matches 112; Conservative 81; Mismatch	INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENCTH: 922 amino acids TYPE: amino acid STRANDEDMESS: single TOPOLOGY: linear US-09-116-473-4		H COS	Alskette Compatible M: DOS SEQ for Windows Vers OBATA: BER: US/09/116,473 7-JUL-1998	1 G Street, NW ngton A BLE FORM:	FORMATION:  T: KOLOGKID, Alex T: Ginty, David INVENTION: SEMAPHORIN F SEQUENCES: B NDENCE ADDRESS: SEE: Banner & Witcoff	2 6-473 ce 4,	Qy 640 SPVAGVGAQDGDYQRPHSAQPADRGYDRPKAVSALATE	Db 551 LRTESPLSTRFIRIYPERATHSGLGLRMELLGCEVEAPTAGPTTPNGNPVHE	Qy 583 RAGRHEYALPLAPPEPEYATPIVERHVLRAHT	Db 522NGSE
KFCPAGCRDVAGDISGNMVDGYRDTS	н -	GRL :	NEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEK	331; DB 4; Le No. 3e-20; matches 166;		01107.74973	76	ωн		KIN RECEPTOR		RGYDRPKAVSALATE 677 :      FQLTGGTTVLATE 630	GLRMELLGCEVEAPTAGPTTPNC	-VERHV	NGSDWKTIMDDSKRKAKSFEGNNNYDTPE
YRDTSLICKAAIH 205	-SSDHPDLITC 158   : :   FPEKYPNSLECTY 175	YGPYCGSMTVPKELLLN 124 :  :   :   :: : WGKFCGKI-APSPVVSS 115	YPGTYPNHTVCEK 70    :         YPHSYHPSEKCEW 56	ngth 922; Indels 106; Gaps 19									NPVHE 602		: :    : KSFEGNNNYDTPE 550
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US-07-607-538C-4
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US-07-607-538C-4
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                                                          Query Match
         Matches
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 943-1931 TELEFAX: (510) 943-1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #10, VI
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/07/607,538C
FILING DATE: 01-NOV-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
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NAME: Viviana Amzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Viviana Amzel REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
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tive 30; Mismatches
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US-08-162-402B-4
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                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                     Matches
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NAME: Amzel, Vividica

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P66

TELECOMMUNICATION INFORMATION:

THE COMMUNICATION INFORMATION:

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                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 46
TITLE OF INVENTION: GL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM
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                   306 NNHKPREWLEIDLGEKKKITGIRTTGSTOSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNE 365
                                                                                             253 NGCSRSLSFE----PDGQIRASS---SWQSVNESGDQVHWSPGQARLQDQGPSWASGDSS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                          LENGTH:
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NNNK--QWIEIDLLKIKKITAIITQGCKSLSSEMYVKSYTIHYSEQGVEWKPYRLKSSMV 168
                                                                NGCSTPLGMENGKIENKQITASSFKKSWW-----GD--YWEPFRARLNAQGRVNAWQAKA 110
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Flower St., 19th Floor
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                                                                                                                                 Score 321; DB 2;
Pred. No. 2.1e-20;
0; Mismatches 51;
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                                                                                                                                                                   Length 218;
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Search completed: May 15, 2003, 13:15:18 Job time: 22.4368 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-746-111-5
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US-08-746-111-5
                                                                                                                                                                                                                                                                                                                                                     Ouery Match 8.4%; Score 318; DB 3; Length 2183; Best Local Similarity 40.8%; Pred. No. 1.8e-18; Matches 69; Conservative 31; Mismatches 53; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 2183 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ingolla, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ginsburg, David
APPLICANT: Cui, Jisong
TITLE OF INVENTION: Compositions And Methods For Screening
TITLE OF INVENTION: Compounds For Anticoagulant Activity
                                                                                        2134 DKIFEGNSNTKGHMKNFFNPPIISRFIRIIPKTWNQSIALRLELFGCDI 2182
                                                                                                                                                                           2076 NNNK--QWLQVDLLKIKKVTAIVTQGCKSLSSEMYVKSYSIQYSDQGVAWKPYRQKSSMV 2133
                                                                                                                                                                                                                                                               2023 NGCSTPLGLEDGRIQDKQITASSFKKSWW-----GD--YWEPSLARLNAQGRVNAWQAKA 2075
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                                                                                                              253 NGCSRSLSFE----PDGQIRASS---SWQSVNESGDQVHWSPGQARLQDQGPSWASGDSS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/746,111 FILING DATE: 06-NOV-1996 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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Perfect score:
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sp_unclassified:*
sp_rvirus:*
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(without alignments)
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Q92G35
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Q9PCB6
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Q8X543
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Q9D696
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                               Q96h40 homo sapien
Q92g35 rickettsia
Q8ypn2 anabaena sp
Q9xex1 gracilaria
Q9h8g1 homo sapien
Q9bze6 homo sapien
Q9bze6 homo sapien
Q96jc4 homo sapien
Q96jc4 homo sapien
Q96abc3 homo sapien
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Q9d696 mus musculu
Q9d4j3 mus musculu
Q8x543 escherichia
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Q9auc3 lycopersico
196dw2 homo sapien
Q9pcb6 xylella fas
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ALIGNMENTS

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	Q9ckb0 pasteurella		Q9kak8 bacillus ha	098023 cercopithec		Q40628 oryza sativ		O80422 oryza sativ			098026 hylobates l	-	Q41069 pisum sativ		Φ	Q8squ6 encephalito	Q21223 caenorhabdi	Q9khb9 erwinia chr	N		a	_	Q97m44 clostridium	Q9hsh4 halobacteri		Q94m38 streptococc	methan	gallus	Q8vxs1 cicer ariet

## RESULT Q9D696 AC Q9 AC Q Query Match Best Local Similarity Matches 01-JUN-2001 (TrEMBLrel. 1 01-JUN-2001 (TrEMBLrel. 1 01-JUN-2002 (TrEMBLrel. 2 4631413K11Rik protein. 4631413K11RIK. Q8R327 Q8R327; Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC056771; AAH26771.1; -. SEQUENCE 432 AA; 46798 MW; AD3FB42B24CD4917 CRC64; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last seque 01-JUN-2002 (TrEMBLrel. 21, Last annot Similar to RIKEN cDNA 4631413K11 gene. Eukaryota; Metazoa; Mammalia; Eutheria; NCBI\_TaxID=10090; Mus musculus (Mouse) Eukaryota; Metazoa; ( Q9D696; Q9D696 SEQUENCE FROM N.A. Mus musculus (Mouse) Conservative 0; PRELIMINARY; PRELIMINARY; Chordata; Rodentia; Chordata; 6.78; 17, 17, 21, Last sequence update) Last annotation update) Created) Last sequence update) Last annotation update) Score 28; Pred. No. Craniata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus PRT; PRT; red. No. 4. 460 432 4.4e-21; hes 0; DB 11; Vertebrata; ₽. ₿ Length 432; Indels Euteleostomi; 0

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RY SEDURENCE FROM N.A.

RY SEQUENCE FROM N.A.

REDLINE-21085660; PubMed-11217851;

RX MEDLINE-21085660; PubMed-11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,

RA Arakawa T., Hara A., Fukunishi T., Konno H., Kasukawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Kadota K., Maisuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Sakai M., Barsh G., Fletcher C., Fujita M., Gariboldi M.,
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Garriboldi M.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garriboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wanga K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
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Q9D4J3;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                         4631413K11RIn.
4631413K11RIn.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AK014521; BAB29409.1; -.
MGD; MGI:1913936; 4631413K11rik.
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01-JUN-2002 (TrEMBLrel.
4631413K11Rik protein.
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InterPro; IPR004043; LCCL_dom.
Pfam; PF00431; CUB; 1.
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E; PS01180; CUB; 1.
GCE 460 AA; 50334 MW;
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28; Conser
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100.0%; Pr
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17,
21,
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Last annotation update)
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Q8X543;
01-MAR-2002
01-MAR-2002
PROSITE;
Complete
SEQUENCE
                                                                                             Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoye Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe TIIda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).

EMBL; AB005598; AAG58866.1; -.
                                                                                                                                                                                                                                                                               Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kikpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Genome sequence of enterohaemorrhagic Escherichia coli O157:H7." "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
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-- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AKO16485; BAB30265.1; --
MGD; MGI:1913936; 4631413K1R1k.
InterPro; IPR000859; CUB_domain.
InterPro; IPR004043; LCCL_dom.
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                                      InterPro; IPR000849; GlpT_transporter.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGREAMs; TIGR00881; 2A0104; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
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                                                                                                                                                                                                                            STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
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 proteome.
                           PS00942; GLPT;
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ilarity 100.0%;
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Last annotation update)
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Pred. No.
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C3442BAC11132448 CRC64;
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ches 0;
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Mombaerts
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Tobe T.,
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Q92G35;
Q1-DEC-2001
                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-MALISH 7;
MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiff
Samson D., Roux V., Cossart P., We
                                                            EMBL; AE008676; AAL03828.1
Hypothetical protein; Comp
SEQUENCE 255 AA; 29018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50805; KRAB; 1.
PROSITE; PS50157; ZINC_FINCER_C2H2_2;
DNA-binding; Zinc_finger.
SEQUENCE 216 AA; 25227 MW; B5C6CF.
                                                                                                                                                                                                                                                                                  Rickettsia conorii.
Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
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Mammalia; Eutheria;
                                                                                                                Science
                                                                                                                                                  Raoult D.;
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                                                                                                                                                                                                                                                                                                                                         Hypothetical
RC1290.
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Submitted (MAY-2001)
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                                                              Mechanisms of evolution in Science 293:2093-2098(2001).
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llarity 100.0%;
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Primates;
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                                                                                                                                                                                                                                                                                    alpha subdivision;
eae; Rickettsia.
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Last
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Last
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Pred. No.
          Score
Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                          proteome.
4E4A58667E03C9B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B5C6CF182AFFCCF2 CRC64;
                                                                                                                                                              iffren P., Fo
Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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annotation update)
м 8;
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.3;
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Q9XEX1
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Best Local S
Matches 8
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01-MAR-2002
01-JUN-2002
                                                                                "Occurrence of closely spaced genes in the nuclear genome agarophyte Gracilaria gracilis.";
submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-I- CATALYTIC ACTIVITY: L-SERINE + 1-(INDOL-3-YL)GLYCEROL.
            InterPro;
InterPro;
                              -!- SIMILARITY: TO THE TRPB
EMBL; AF121272; AAD17312.1;
HSSP; P00933; 2WSY.
                                                              - L-TRYPTOPHAN + GLYCERALDEHYDE 3-PHOSPHATE +
-I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY)
-I- PATHWAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; irnverse; 1.

Pfam; PF02143; Radical_activat; 1.

Hypothetical protein; Complete proteome.

Yea AA: 29421 MW; BDF27F3428A007D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakazaki N., Shimpo S., Sugimoto M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the fil-
cyanobacterium Anabaena sp. strain PC
cyanobacterium Anabaena sp. strain PC
DNA Res. 8:205-213(2001).
EMBL; AP003595; BAB75860.1;
InterPro; IPR001989; Radical_activat.
                                                                                                                                                                         NCBI_TaxID=2777;
                                                                                                                                                                                     Gracilaria.
                                                                                                                                                                                              Eukaryota; Rhodophyta; Florideophyceae;
                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. Tryptophan synthase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-21595285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical ALR4161.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           01-NOV-1999
                                                                                                                                                                                                                                                               Q9XEX1;
                                                                                                                                                                                                                                                                           Q9XEX1
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Pro; IPR000993; PF00291; PALP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  =21595285; PubMed=11759840;
T., Nakamura Y., Wolk C.P., K.
P., Iriguchi M., Ishikawa A.
P., Kohara M., Matsumoto M.,
N., Shimpo S., Sugimoto M.,
                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conser
                     1PR001926;
                                                                                                                                                                                                                                        (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
; B6_enzyme_beta.
; Trp_synth_beta.
; 1.
                                                                                                                                                                                                                                                                                                                                                                                    1.9%;
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. 12, Last sequence upd
. 20, Last annotation u
C 4.2.1.20) (Fragment).
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                                                      FAMILY.
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Last annotation update)
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Pred.
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                                                                                                                                                                                                                     (Fragment).
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Takazawa
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                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
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Kawashima
                                                                                                                                                                                               Gracilariales;
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                                                                                                                                                                                                                                                                                                                                                                                             Length 264;
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Muraki A.,
                                                                TRYPTOPHAN
                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 10
Q9BZE6
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Best Local S
Matches 8
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Best Local S
Matches 8
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Pfam; PF00096; zf-C2H2; 3.
ProDom; PD000003; Znf_C2H2; 2.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 3.
PROSITE; PS50805; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PLACENTA;
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA seguencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO3721; BAB14656.1; -.
                                                                        01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSUULDO, L...Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ13659 fis, clone PLACE1011576, moderately similar to
kruppel related zinc finger protein (HTF10) mRNA.
                                                          KRAB zinc finger
     Eukaryota;
                         Homo
                                                                                                                                      Q9BZE6;
                                                                                                                                                       Q9BZE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9H8G1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9H8G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO01909; KRAB.
                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro;
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                                                                                                                                                                                                                                                     82
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                         sapiens
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00028;
PS50157;
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                               550805; KRAB; 1.
500028; ZINC_ENGER_C2H2_1; 2.
550157; ZINC_FINGER_C2H2_2; 3.
550157; Jinc_FInger.
9; Metal-binding; Zinc-finger.
364 AA; 42472 MW; 5043DA4C575842B0 CRC64;
     Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA;
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                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             Conservative
                       (Human)
                                                                                                                                                                                                                                                                                        126
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                                                          protein
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   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37422 MW;
                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                          17, Created)
17, Last sequence update)
21, Last annotation update)
n HZF26 (Fragment).
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Pred. No. 13;
0; Mismatches
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   Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                              DB 4;
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   Euteleostomi;
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                                                                               RA Watanabe M., Fujimori K., Yosida M., Watanabe S., Ishida S., Ono Y.
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.
RA Sugiyama T., Irle R., Otsuki T., Sato H., Wakamatsu A., Ishida Y.
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Rikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RI "NEDO human cDNA sequencing project.";
RI Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databasor-
NR InterPro; IPR001909; KRAB.
R InterPro; IPR001909; KRAB.
     A ID

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Best Local S
Matches
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finger protein 91.
Homo sapiens (Human).
Horvota; Metazoa; Chordata; Cr
InterPro; IPRO01909; KRAB.
InterPro; IPRO0822; Znf_C2H2.
Pfam; PP01352; KRAB; 1.
Pfam; PF00096; zf-C2H2; 12.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50805; ZINC_FINGER_C
PROSITE; PS50157; ZINC_FINGER_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096M04 PRELIMINARY; PRT; 519 AA.
096M04;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ32933 fis, clone TESTI2007466, moderately similar
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DNA Cell
[2]
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Abrink M., Aveskog
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ZINC_FINGER_C2H2_1;
ZINC_FINGER_C2H2_2;
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   UNKNOWN_8.
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Hominidae;

Euteleostomi;

б

zinc

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Abrink M., Aveskogh M., Hellman L.;
"Isolation of cDNA clones for 42 different Kruppel-related proteins expressed in the human monoblast cell line U-937."
DNA Cell Biol. 14:125-136(1995).
                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                            Hellman L.;
the EMBL/GenBank/DDBJ databases.
N: NUCLEAR (BY SIMILARITY).
                                               997CB1C95D37E983 CRC64;
 Mismatches
                       DB
                                                                     Zinc-finger
 0
                     Length
                        470;
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0
Gaps
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RESULT 13
Q96BB5
ID Q96BB
AC Q96BB
DT Q1-DE
DT Q1-DE
DT Q1-MA
DE Hypot
OS HOMO
OC ELLKAI
OC MARMA
OX NCBI.
RN [1]
RP SEQUE
RC TISSE
RA SETAM
DR Inte
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29 ESULP

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Best Local S
Matches 8
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*Molecular cloning and preliminary functional analysis of

*Molecular cloning and preliminary functional analysis of

human KRAB zinc finger proteins, HKr18 and HKr19.*;

DNA Cell Biol 20:275-286(2001).

EMBL; AP277624; AAX61307.1; -

InterPro; IPR001909; KRAB.

InterPro; IPR001909; KRAB.

InterPro; IPR000822; Znf_C2H2.

Pfam; PP01352; KRAB; 1.

PROSITE; PS50005; KRAB; 1.

PROSITE; PS50028; ZINC_FINGER_C2H2_1; UNKNOWN_11.

PROSITE; PS50028; ZINC_FINGER_C2H2_1; INKNOWN_11.
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01-DEC-2001
01-DEC-2001
01-MAR-2002
Strausberg R.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ
EMBL; BC015765; AAH15765.1; -.
InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf_C2H2.
                                                                                        TISSUE-B-CELL;
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Mammalia; Eutheria;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Hypothetical 61.9 kDa protein.
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524 AA;
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Mammalia; Eutheria;
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SEQUENCE 519 AA; 60350 MW;
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8; Conserv
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Metazoa; Primates; (
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24 AA; 60598 MW;
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Primates;
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Catarrhini;
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Catarrhini;
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i; Hominidae;
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Q96DW2
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Pfam; PF00560; LRR; 5.
Pfam; PF00069; pkinase; 1.
Probom; PD000001; Euk_pkinase;
PT00000; PD000001; LRR; 5.
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Pfam; PF00096; zf-CzH2; 13.
PROSITE; PS00026; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_13.
PROSITE; PS00128; ZINC_FINGER_C2H2_2; 13.
DNA-binding; Hypothetical protein; Zinc-finger.
DNA-binding; Hypothetical protein; Zinc-finger.
SEQUENCE 536 AA; 61932 MW; 3DC80FAE55F8CC00 CRC64;
                                                                                                                                                                                                                                                                                        SMART; SM00370; LRR; 5.
SMART; SM00220; S_TKC; 1.
SMART; SM002219; TYTKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 612 AA; 68096 MW; A39B3C37751C3F27 CRC64;
            01-DEC-2001 (TIEMBLIFE: 19, 01-DEC-2001 (TIEMBLIFE: 19, 101-JUN-2002 (TIEMBLIFE: 21, 11) similar to RecQ protein-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression patterns during pollen tube growth Submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AF243040; AAK28345.1; -
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                           Q96DW2;
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*New pollen-expressed receptor kinases
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InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
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InterPro; IPR001245;
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(Human).
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Tyr_pkinase.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBL_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RP STRUSBERG R.;
SUBMITED (AUG-2001) to the EMBL/GenBank/DDBJ databases.

RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

DR Interpro; IPR001410; DEAD.
DR Interpro; IPR001410; DEAD.
DR Interpro; IPR001410; DEAD.
DR Interpro; IPR00150; Helicase_C; 1.

KW ATP-binding; Helicase_C; 1.

KW ATP-binding; Helicase_C; 1.

KW ATP-binding; Helicase_C; 1.

KW ATP-binding; Helicase_C; 1.

SQ SEQUENCE 657 AA; 73415 MW; CF51B910F560CA18 CRC64;

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Query Match
SEQUENCE 657 AA; 73415 MW; CF51B910F560C
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Title:
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C. glutamicum LP-6	Corynebacterium gl	Chlamydia pneumoni	Human neuropilin-H	Human polypeptide,	Listeria monocytog	Human olfactory re	Novel bone marrow		Novel human diagno	P. pantotrophus GB	Rice carbonic-anhy	Streptococcus poly	Corynebacterium gl	C glutamicum prote	Drosophila melanog	C glutamicum prote			Human secreted pro	Propionibacterium	æ			Human polypeptide	Corynebacterium gl		Human protein sequ		_	_	_	immune/ha	MDDT SE	Human protein sequ

# ALIGNMENTS

AAU00630
ID AAUC
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AC AAUC

AAU00630 standard; Protein; 539 Ä

AAU00630

29-AUG-2001 (first entry)

Novel human protein (NHP) sequence #3.

Novel human protein; NHP; CUB domain; extracellular domain; gene therapy; obesity; high blood pressure; connective tissue disorder; infertility; NHP-mediated pathway.

Homo sapiens.

WO200129219-A1

26-APR-2001.

08-OCT-2000; 2000WO-US28798.

19-OCT-1999; 99US-0160285. 18-FEB-2000; 2000US-0183583.

(LEXI-) LEXICON GENETICS INC

Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz

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Sands

AT;

WPI; 2001-290917/30. N-PSDB; AASO0615.

Novel nucleic acid encoding human CUB-domain containing protein, useful

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RESULT 2
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                           Novel human protein; NHP; CUB domain; ext obesity; high blood pressure; connective NHP-mediated pathway.
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diseases -
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Matches 418
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N-PSDB; AASO0614.
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18-FEB-2000; 2000US-0183583.
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DB; AAS00613.
                                                                                                                                 GSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSK
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                                                                                                                                                                                                                                                                                                                                                                                                    400;
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pressure; connective tissue disorder; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHP-mediated pathways.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neuropilin-like polypeptide; neuropilin-Hyl; neovascularisation; (W neurodegenerative disease; Alzheimer's disease; learning; angiogenesis; (W thrombocytopaenia; memory; platelet; plastic anaemia; antiinflammatory; (W ophthalmological; paroxysmal nocturnal haemoglobinuria; protozoacide; (W wound healing; tissue repair; Parkinson's disease; Huntington's disease; (W amyotrophic lateral sclerosis; Shy-Drager syndrome; trauma; spinal cord; (W cerebrovascular; stroke; ulcer; immune; infection; multiple sclerosis; (W human immunodeficiency virus; HIV; autoimmune disorder; dermatological; (W systemic lupus erythematosus; rheumatoid arthritis; antithyroid; cancer; autoimmune thyroiditis; diabetes mellitus; graft-versus-host disease; (W myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; (W nootropic; neuroprotective; tranquilliser; virucide; antibacterial; cytostatic; (W immunosuppressive; chromosome 6q21.
                                                                                                                                     Novel isolated human Neuropilin-Hyl and Neuropilin-Hyl polypeptides useful for treating neurodegenerative diseases e.g. Alzheimer's
                                                                                                                                                                                                                      Tang
                                                                                                                        disease,
                                                                                                                                                                              WPI; 2002-393966/42.
N-PSDB; AAD35992.
                                                                                                                                                                                                                                                                             11-SEP-2000;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                      12-SEP-2001; 2001WO-US28488
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                             2000US-0659671.
2001US-317902P.
                                                                                                                                                                                                                                                   INC
                                                                                                                      diagnosing and
                                                                                                                     mapping genetic neuronal defects
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The invention relates to neuropilin-like polypeptide (neuropilin-Hyl and neuropilin-Hyl) and their corresponding nucleic acids. The neuropilin-like polypeptides and polypucleotides are useful in modulating neuronal growth regenerative capacity, treating neurodegenerative diseases, diagnosing and mapping genetic neuronal defects and degenerative disease like Alzheimer's disease and for treating learning and memory disorders.

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Claim 3;

Page 123-125; 152pp;

English.

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerve regeneration; neurodegenerative disease; learning disorder; memory disorder; Alzheimer's disease; ampiogenesis; neovascularisation; organ growth; nervous system lesion; cancer; cell proliferation; cell differentiation; stem cell growth factor activity; parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; haematopoiesis; myeloid cell disorder; lymphoid cell disorders; anaemia; platelet disorder; thrombocytopaenia; liver fibrosis; lung fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelet disorders e.g. thrombocytopaenia, plastic anaemia and parox nocturnal haemoglobinuria and is used in nerve tissue growth or regeneration, in wound healing, tissue repair and replacement and in healing of bones, incisions and ulcers. Compositions comprising the healing of bones, incisions and ulcers. Compositions comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                They are also useful for inducing angiogenesis, neovascularisation, well as organ growth and development e.g. heart and other tissues. Antagonists of neuropilin-like polypeptides are useful for treating cancers and other malignant diseases. Neuropilin is used to treat
WPI; 2002-351881/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; neuropilin-Hy1; chromosome 6q21; neuronal growth;
nerve regeneration; neurodegenerative disease; learning disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                         Tang TY;
                                                                                                                                                                                   11-SEP-2000;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                         WO200222780-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Neuropilin-Hyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2002
                                                                                                                                                                                                                                                                                11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reperfusion;
                                                                                                                      (TANG/) TANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYASSDHP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYASSDHP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 AA;
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                                                                                                                                                                                   2000US-0659671.
2001US-0659671.
                                                                                                                                                                                                                                                                                2001WO-US28590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food supplement; DNA microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 116;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
2e-106;
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New neuropilin-like polypeptides for diagnosing, treating neurological conditions and disorders, o
                                                                                                                                                            N-PSDB; ABK49565
                                                                                                                                             inducing angiogenesis and neovascularisation
                                                                                                                                                 cancers,
                                                                                                                                                     preventing and
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Claim **ω** Page 118-120; 144pp; English.

Control of the cDNAs are useful for proteins and encoding cDNAs are useful controlled co gene chips and as a DNA antigen. The present sequence represents encoding the proteins and the coding regions of the cDNAs. Also included is a nucleic acid array comprising the cDNAs attached to a surface used for detecting full-matches or mismatches to the cDNAs. The genes for neuropilin-Hyl and Hy2 are located on human chromosome 6q21. The nucleic acid array is useful for detecting full-matches or mismatches The neuropilin-Hyl. invention ion relates to neuropilin-Hy1 an isolated neuropilin-like polypeptide and neuropilin-Hy2, the full length cDNAs

Sequence 398 A,

Best Local Similarity Matches 116; Conserv Query Match Conservative 27.8%; 0; Score 116; Pred. No. Mismatches 2e-106; thes 0; DB Length 398 Indels 0; Gaps 0

4 GDGCGHLVTYQDSCTMTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASD 63

GDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASD

63

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4

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RESULT 6 AAB19126

AAB19126 standard; Protein; 503

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AAB19126

19-FEB-2001 (first entry)

Polypeptide isolated from lymph node stromal cells of <u>'</u>

cardiac immune system disorder; can blood vessel growth; tumour inflammatory bowel disease; Lymph node stromal cell; fsn -/- mice; failure. ell; fsn -/- mice; inflammatory disorder; er; cancer; viral disorder; HIV infection; tumour necrosis factor disorder; arthritis; isease; fibroblast growth factor-mediated di disorder;

Mus **q**s

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a polypeptide sequence which is isolated from lymph node stromal cells of fsn -/- mice. The polypucleotides and their polypeptides are useful for treating an inflammatory disorder, disorder of immune system and cancer selected from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a viral disorder, in particular HIV infection and for modulating the growth of blood vessels. The polypeptides are useful for treating a tumour necrosis factor (PNF) mediated disorder, such as those selected from arthritis, inflammatory bowel disease and cardiac failure and a fibroblast growth factor-mediated disorder. It is also useful in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, to quantify levels of protein or cognate corresponding ligand or receptors, as antiinflammatory agents, and in compositions for the treatment of skin, connective tissue and tissue, as a chromosome marker or tags in the identification of a genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                            Matches
             WO200162927-A2
                                                                               cell proliferative acquired immune def
                                                                                                                                      Human diagnostic and therapeutic polypeptide (DITHP) #53.
                                                                                                                                                                     04-DEC-2001
                                                                                                                                                                                                                             AAU19467 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide expressed in mammalian fsn -/- lymph node stromal cells, useful for modulating growth of blood cells, for treating inflammatory and tumour necrosis factor-mediated disorders, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strachan L,
Murison JG;
                                        Homo sapiens.
                                                                                                                                                                                                  AAU19467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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26-AUG-1999;
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                                                                  respiratory disorder.
                                                                                                                                                                                                                                                                                                 (GENE-) GENESIS RES & DEV CORP LTD.
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DB; AAA96736.
                                                                              receptor; diagnostic; therapeutic; gene therapy; vaccine; rollferative disorder; Crohn's disease; lymphoma; leukaem! ed immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 68-69;
                                                                                                                                                                                                                                                                                                                                                                                                                       503
                                                                                                                                                                                                                                                                                                                                                         6.7%; S ilarity 100.0%; Conservative 0;
                                                                                                                                                                    (first entry)
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99US-0383586
                                                                                                                                                                                                                             Protein; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M, Abernethy N,
                                                                                                                                                                                                                                                                                                                                                         Score 28; DB; Pred. No. 6.8
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                                                                                                                                                                                                                                                                                                                                                                      DB 21; I
6.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                     Length 503
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                                                                                             leukaemia;
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The invention relates to polynucleotides (I) encoding diagnostic and Ct therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, CC and proteins involved in growth and development and receptors. (I) and CC (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and CC (II) may be used to treat disorders associated with decreased polypeptide (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, CC or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, CC crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, CC (I) may be used to produce the DITHPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative
                                                                                                                                                                                                                                                                                                                                                                                                                       Dufour GE,
Liu TF, Ro
Wright RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                     Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-502867/55.
N-PSDB; AAS31038.
                                                                                                                                                                                                                                                                            Claim 27; Page 430; 522pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panzer SR,
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24-FEB-2000;
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CE, Flores V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                          Roseberry AM;
J, Yap PE, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spiro PA,
Sa SA, Ams
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2000US-0204908.
2000US-0205232.
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s V, Fong WT, G
y AM; Rosen BH,
                                                                                                                                                                                                                                                                                                                                                                                                              DM,
                                                                                                                                                                                                                                                                                                                                                                                             Banville SC, Shah P, CHALLY ..., nshey S, Dahl CR, Dam TC, Daniels SE; Fong WT, Greenawalt LB, Hillman JL, Jc M; Rosen BH, Russo FD, Stockdreher TK, I Yu JY, Bradley DL, Bratcher SR, Chen W; M; Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones 1
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RESULT 8
ABP51369
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Best Local :
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06-SEP-2000
06-SEP-2000
06-SEP-2000
06-SEP-2000
06-SEP-2000
06-SEP-2000
06-SEP-2000
06-SEP-2000
06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                          Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; ALDS; autoimmune disorder; inflammatory disorder; allergy; multiple scleros; rheumatoid arthritis; transgenic; gene therapy; antiarteriosolerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies against DITHPS and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAU19415-AAU19625 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention.
                                                                                                                                                                                                                                                                               06-SEP-2000;
06-SEP-2000;
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N-PSDB; ABQ72586
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MDDT SEQ ID NO
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           2002-527544/56
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                                                 MG,
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8; Conser
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                                                                       Lincoln SE,
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llarity 100.0%;
Conservative
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                                         Peralta CH
                                                                                                                                                  2000US-230988P.
2000US-230989P.
                                                                                                                                                                                 2000US-230598P.
2000US-230599P.
2000US-230610P.
                                                                                                                              2000US-230951P.
2000US-231163P.
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                                                     Bradley
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                                                                                              GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic;
                                                              Wright RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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                                                                      Altus CM,
                                         David
                              Rohatgi SD, Harris
David MH, Panzer SR,
g SC, Au AP, Inman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
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Pred.
                                                             Gietzen D,
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  antiarthritic.
                                                                       Dutour GE,
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11;
                                                              Liu
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                                 3 B, no Flores
                                                          TF,
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                                RR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 101;
                                                                        Chalup MS,
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                                                   Roseberry
                                                              Yap PE,
                                                                         Hillman
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                                                            Dahl CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                          sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                            antigout;
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Sequence

101

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CC polynuclectide comprising. Oligonuclectides and antibodies are useful for CC detecting MDDT in a sample or for assessing toxicity of a test compound, CC in a diagnostic test for a condition or a disease associated with the CC expression of MDDT in a biological sample, for detecting (I) in a sample, CC and for purifying (I) from a sample. A composition comprising (I), an CC agonist or antagonist is useful for treating a disease or condition CC associated with decreased or increased expression of functional MDDT. CC (I) or (II) are useful for diagnosing, treating or preventing disorders are sected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, and cancer and an CC elected from a cell proliferative disorder such as arteriosclerosis or Theumatolid arthritis. (II) are useful for creating knockin humanised CC allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or CC elected from a characy, to generate a transcript image of a tissue or cell cype, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology. Nucleic acids (II) (AB072449-AB072700) encoding (I) are useful for screening a compound for effectiveness in altering expression of a target screening a compound for effectiveness in altering expression of a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment (MDDT) polypeptide (I) selected from a polypeptide sequence selected from 254 sequences (ABP51231-ABP51484) give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 541-542; 618pp; English
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Best Local
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                                                         Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antipsoriatic; antiatherosclerotic; antipsoriatic; antiatherosclerotic; antique; neuroprotective; antirheumatic; antiarthritic.
                                   Homo sapiens
                                                                                                                                                                                                                                    ABP51461 standard; Protein;
                                                                                                                                                             Human MDDT
                                                                                                                                                                                     03-SEP-2002
                                                                                                                                                                                                              ABP51461;
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8; Conser
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Jurity 100.0%;
Conservative c
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s; Pred. No. 11;
0; Mismatches
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11;
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The invention relates to an isolated human disease detection and CC treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51331-ABP51484) given in the Sequence specification, a naturally occurring polypeptide comprising a sequence CC immunogenic fragment of (I). (I) or a biologically active or CC immunogenic fragment of (I). (I) is useful for screening a compound for CC preparing a polyclonal or monoclonal antibody by hybridoma technology. CC Nucleic acids (II) (AB072449-AB072700) encoding (I) are useful for CC polynucleotide comprising. Oligonucleotides and antibodies are useful for CC expression of MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the CC expression of MDDT in a biological sample, for detecting (II) an sample, CC and for purifying (I) from a sample. A composition comprising (I), an associated with decreased or increased expression of functional MDDT. CC associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, associated with aberrant expression of MDDT, where the disorders are consociated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, continuals or transgenic animals to model human disease, in somatic or rheumatoid arthitis. (II) are useful for creating whockin humanised or troe differences in the chromosomal location due to
                                            germline gene therapy, to generate a transcript for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals translocation or inversion among normal, carrier or affected individuals
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06-SEP-
06-SEP-
06-SEP-
06-SEP-
06-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. AIDS
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Gerstin EH,
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06-SEP-2000;
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06-SEP-2000;
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06-SEP-2000;
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DB; ABQ72678:
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2000US-230514P.
2000US-230515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JY. Wright RJ, Gietzen D, Liu TF, Yap PE, Bradley DL, Rohatgi SD, Harris B, Roseberry Peralta CH, David MH, Panzer SR, Flores V, D then AJ, Chang SC, Au AP, Inman RR;
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2000US-230989P.
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2000US-230865P.
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2000US-230598P.
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2000US-230595P.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and thempay, drug screening, assays for recontractivity activity and status and thempay.

Novel nucleic acids and polypeptides, useful such as central nervous system injuries -

for

treating disorders

Example

3; SEQ ID NO 2091; 10078pp; English.

c.N.S disorders.

sequence data for this patent did

not form part of the printed

activity, arthritis

inflammation,

leukaemias and

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RESULT 10
AAM38946
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Best Local Similarity
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                                                                                                                                                                                                                                             21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                    Wang
                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                       WPI; 2001-442253/47.
N-PSDB; AAI58102.
                                                                                                                                                                                                         (HYSE-)
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                                                                                                                                                                                                                                                                                                                       WO200153312-A1
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                       Human
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                                                                                                                                                                                                                                                                                                                                                     leukaemia.
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                                                                                                                                                                            Wang Z,
Zhou P,
                                                                                                                                                                                                          DESAH
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman T, 7
Goodrich R,
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Pred. No.
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Yang Y,
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Chalup

Daffo A; Z Dahl CR;

specification

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RESULT 11
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Best Local
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         of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence,3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs -
                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 11667; 2537pp + CD ROM; English
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2000JP-0183767.
2000JP-0241899.
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T, Wakama
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A, Nagai K,
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12;
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Ctsuki
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AAH13629 tc
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Best Local
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                                                                                                                                                                                   06-SEP-2000

06-SEP-2000

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06-SEP-2000

06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; ADDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antificammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiallergic; antianaemic; antiatherosclerotic; antique; neuroprotective; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                       Jackson
                                                                                                                                            (INCY-)
                                                                                                                                                                                                                                                                                                                                                      06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                               WO200240715-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP51401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDLITCLE
                                                                                                         . S,
                                                                                                                                            INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA;
                                                                                                                                                                                                       2000US-230505P.
2000US-230514P.
2000US-230514P.
2000US-230517P.
2000US-230519P.
2000US-230519P.
2000US-23059P.
                                                                                                          Lincoln SE, Altus
Zu JY, Wright RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                      2001WO-US27628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                                                       Altus CM,
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0%
;
                                                                                       Itus CM, Dufour GE, Chalup I
RJ, Gietzen D, Liu TF, Yap
Rohatgi SD, Harris B, Rosel
David MH, Panzer SR, Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No.
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                                                                                  Chair
u TF, Yap Pb,
a, Roseberry /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                      Hillman
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Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder

e.g.

Gerstin Momiyama MG,

EH,

Bradley DL, Rohatgi : Peralta CH, David MH,

Marwaha

Chen AJ,

Chang

SC,

Ą AP,

RR;

Dahl

N-PSDB;

2002-527544/56. DB; ABQ72618.

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RESULT 13
AAM90976
ID AAM90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC specifically binds (I) or modulates the activity of (I), and for CC preparing a polyclonal or monoclonal antibody by hybridoma technology. CC Nucleic acids (II) (AB072449-AB072700) encoding (I) are useful for CC screening a compound for effectiveness in altering expression of a target CC polynucleotide comprising. Oligonucleotides and antibodies are useful for CC detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the CC expression of MDDT in a biological sample, for detecting (I) in a sample, and for purifying (I) from a sample, a composition comprising (I), an CC agonist or antagonist is useful for treating a disease or condition CC associated with decreased or increased expression of functional MDDT. CC (I) or (II) are useful for diagnosing, treating or preventing disorders are Selected from a cell proliferative disorder such as arteriosclerosis, cc altergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or CC altergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or CC animals or transgenic animals to model human diseases, in somatic or cell type, for detecting differences in the chromosomal location due to CC translocation or inversion among normal, carrier or affected individuals and both which test the proposed for manylog and the chromosomal location due to cardinate the hybridistic proposed for manylog normal, carrier or affected individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
31 JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound the specifically binds (I) or antagonist, for screening a compound the specifically binds (I) or modulates the activity of (I) and for
                                                                                                                   17-JAN-2001;
                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                    WO200157182-A2
                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematop
cytostatic; gene therapy; vaccine; metastasis
                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                     07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                      AAM90976;
                                                                                                                                                                                                                                                                                                                                                                                                  AAM90976 standard; Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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90 PDLITCLE 97
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les 8; Conserv
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                                                                                                                                                                                                                                                                                                   immune/haematopoietic antigen
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                   2001WO-US01354
                                                                                                                                                                                                                                                                  haematopoietic; immune/haematopoietic antigen; cancer;
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100.0%; Pr
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Pred. No.
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                                                                                                                                                                                                                                                                                                   SEQ ID NO:18569
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o. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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that
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   25-SEP-2000
26-SEP-2000
27-SEP-2000
27-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
02-OCT-2000
02-OCT-2000
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14-SEP-2000;
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01-SEP-2000;
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14-AUG-2000;
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2000US-0205515.
2000US-0209467.
                                                                                                                               2000US-0236369
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2000US-0234274
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Nucleic acids encoding useful for preventing, metastasis -
             Claim 11; SEQ ID NO 18569; 3071pp + Sequence Listing; English
                                              N-PSDB;
                                                                        ( HUMA - )
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                                              2001-483426/52.
DB; AAK63757.
                                                                        HUMAN GENOME
                                                             Barash SC,
                                                                                       2000US-0251990
2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                              2000US-0240960.
2000US-0241221.
                                                                                                                                                                                                                                             2000US
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-0249218.
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                                                                                                                                                                                    0249244.
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                                                                        SCI INC
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249210
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249215.
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                                                                                                                                                                                                                                                                                                                          46476.
                                                                                                                                                                                                                                                                                                                                     46474.
                             human immune/hematopoietic antigen diagnosing and/or treating cancers
                                                             MS
                              polypeptides,
and
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amino

acid

sequences

encode the human immune/haematopoietic antigen (I) given in AAM82170 to AAM91921. (I) have cytostatic

Claim 20; Page 293; 6221pp; English.

AAK54951 to AAK64702

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RESULT 14
AAM79595
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Best Local S
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                                                                                       Tang YT,
Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                  03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                                                                                                                                                                             15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopolitic-related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK8764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                             WPI;
                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM79595 standard; Protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                  (HYSE-)
                                                                                                                                                                                                                       01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                     WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein SEQ ID NO 3241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM79595;
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|||||||
20 ASDYLLFT 27
                                              2001-476283/51.
DB; AAK52728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 1.9%; Score 8; DB Similarity 100.0%; Pred. No. 14 8; Conservative 0; Mismatches
                                                                                                                                                HYSEQ INC.
                                                                                    Liu C,
Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                   ytokine; cell proliferation; cell differentiation; gene therapy;
peptide therapy; stem cell growth factor; haematopoiesis;
rowth factor; immunomodulatory; cancer; leukaemia;
system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                           2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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2000US-0560875.
2000US-0598075.
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                                                                                       Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
). 14;
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F, c
                                                                                                      u P,
Chen
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Wang
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ang ZW;
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119

PDLITCLE 126 PDLITCLE

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Search completed: May 15, Job time: 45.6531 secs

2003, 13:22:39

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ARESULT 15
AAM40732
ID AAM40732
AC AAM40
XX AAM40
XX AAM40
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XX Human
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XX AAM40
XX AAM4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0652191.

19-CCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
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                                                  Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokinetic;
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DB; AAI59888.
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Zhou P,
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Wehrman T, X
Goodrich R,
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, Xu C, Xue
R, Drmanac R
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y; central nervous system; CNS;
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Yang Y,
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Example 2;

SEQ ID NO 5663; 10078pp; English.

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Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213). With nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Inmune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S discreters
                                                                                                                                        C.N.S disorders.
Note: The sequence data
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Sequence 4, Appli
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Sequence 51, Appli
Sequence 6397, Ap
Sequence 6397, Ap
Sequence 5807, Ap
Sequence 4484, Ap
Sequence 148, Appli
Sequence 148, Appl
Sequence 148, Appl
Sequence 114, Appl
Sequence 1, Appli
Sequence 21, Appl
Sequence 1053, A
Sequence 1524, Ap
Sequence 19, Appl
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Sequence 1, Appli
Sequence 20
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4	Sequence 202, App	Sequence 2, Appli	56,	Sequence 56, Appl	854		Sequence 4, Appli	Sequence 27, Appl		33694	132,	230	Sequence 97, Appl	929,	Sequence 262, App	Sequence 48692, A	Sequence 503, App	Sequence 1529, Ap	Sequence 911, App	Sequence 171, App	64,	Sequence 10, Appl	41	Sequence 23, Appl	Sequence 183, App

### ALIGNMENTS

US-09-759-130B-76 Sequence 76, Appropriate Publication No.

Application US/09759130B

APPLICANT:

Barnes, Inchia: Kirst, Susan J Fraser, Christ Sharp, John D McCarthy, Sean of Praser, Christopher C

Thomas S

APPLICANT:

APPLICANT:

APPLICANT: Millennium Pharmaceuticals, APPLICANT: McCarthy, Sean A APPLICANT: Fraser, Christopher C

Inc.

APPLICANT:

Wrighton, Nicolas

Leiby, Kevin R

PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR ETILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR EILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159 PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29 CURRENT APPLICATION NUMBER: US/09/759,130B CURRENT FILING DATE: 2002-09-16 APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES FILE REFERENCE: MPI00-5350MNIM APPLICATION NUMBER: US 09/608,452
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/393,996
FILING DATE: 1999-09-10
APPLICATION NUMBER: US 09/602,871 Goodearl, Andrew THERAPEUTIC, AND OTHER

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-76
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 75, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 76
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Best Local Similarity
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                                                                                                                                                                   TITLE OF INVENTION: NOVEL TITLE OF INVENTION: PROGN
                                                                                                                        CURRENT APPLICATION NUMBER: US/09/759,130B CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Millennium Pharmaceuticals, APPLICANT: McCarthy, Sean A
                                                            PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
                                                                                          PRIOR APPLICATION NUMBER: US 09/479,249 PRIOR FILING DATE: 2000-01-07
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                                            PRIOR APPLICATION NUMBER: US 09/578,063
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                 APPLICATION NUMBER:
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INVENTION: NOVEL GENES
INVENTION: PROGNOSTIC,
                                                                                                                                                                                                                                                                                                                                             Mackay, Charles R
Myers, Paul S
                                                                                                                                                                                                                                                                                                            Kirst, Susan J
                                                                                                                                                                                                                                               Wrighton, Nicolas
                                                                                                                                                                                                                                                                                                                            Barnes, Thomas S
                                                                                                                                                                                                                                 Goodearl, Andrew
                                                                                                                                                                                                                                                                 Leiby, Kevin R
                                                                                                                                                                                                                                                                                                                                          Sharp, John D
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иМВЕR: US 09/333,159
1999-06-14
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Pred. No. 0;
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                  SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: Gao, Zeren
APPLICANT: Shoemaker, Kimberly
TITLE OF INVENTION: NEUROPILIN H
                                                               CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/249,004
PRIOR FILING DATE: 2000-11-15
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PRIOR
                                PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Wil
                                                                                                                                      FILE REFERENCE: 00-62
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TYPE: PRT
ORGANISM: Homo sapiens
LENGTH: 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: UFILING DATE: 1999-06-
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                                    for Windows Version
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                                                                                                                                                    HOMOLOG ZCUB5
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Pred. No. 0;
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TYPE: PRT ORGANISM: Mus

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                                                                                                                  ; ORGANISM: Mus musculus US-10-003-132-6
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                                                                                                                                               SEQ ID NO 6
LENGTH: 458
TYPE: PRT
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10003132 Publication No. US20020192750A1 GENERAL INFORMATION:
                                                            Matches
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LENGTH: 503
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APPLICANT: Gao, Zeren
APPLICANT: Shoemaker, Kimberly E.

TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCUB5
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                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/249,004
PRIOR FILING DATE: 2000-11-15
NUMBER-OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000,1037c3
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                   FILE REFERENCE: 00-62
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ORGANISM: Mouse
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125 SGSHISGRGFLLTYASSDHPDLITCLER 152
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100.0%; Pr
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Pred. No
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Best Local Similarity
7; Conserve
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                                                              FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
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SOFTWARE: PatentIn ver. 3.
SEQ ID NO 6397
LENGTH: 206
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 SEQ ID
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               PRIOR FILING DATE: 2000 NUMBER OF SEQ ID NOS: 70 SOFTWARE: Patentin ver.
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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NO 5807
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IKEDA, MASATO
OZAKI, AKIO
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IKEDA, MASATO
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OCHIAI, KEIKO
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TATEISHI, NAOKO
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OCHIAI, KEIKO
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Pred. No. 70;
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Best Local Similarity
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US-09-738-626-4484
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                                                                                                                                                                                                        Sequence 2, Application US/09909849
Patent No. US20020106754A1
GENERAL INFORMATION:
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SEQ ID NO 4484
LENGTH: 299
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 383
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
;-09-909-849-2
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Best Local Similarity
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                                                                                                                        CURRENT APPLICATION NUMBER: US/09/909,849
CURRENT FILING DATE: 2001-07-23
                                                                                                                                                       APPLICANT: Tauch, Andreas
TITLE OF INVENTION: Nucleotide Sequences Which Code for the alr Gene
FILE REFERENCE: 032301 WD 173
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PRIOR FILING. DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                          NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                    82 TYPKELL 88
                                                                                                                                                                                                                                                                                                                                    16 TVPKELL 22
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TATEISHI, NAOKO
SENOH, AKIHIRO
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RESULT 11
US-09-910-186A-14
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US-09-712-363-148
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 385
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/910,186A CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: PCT/US00/12890
                                                                                                                                                                                                                                                                         APPLICANT: U.S. Army Medical Research & Material Command TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM TITLE OF INVENTION: NUBROTOXIN FILE REFERENCE: A33626-A 067252.0107
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PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
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PRIOR FILING DATE: 2000-01-28
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CURRENT FILING DATE: 2000-11-13
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APPLICANT: MATCOTTO, SECWARD H.
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY C
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                                                                          PRIOR APPLICATION NUMBER: 09/611,419
                                                                                                                        PRIOR FILING DATE:
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FILING DATE: 2000-07-06
APPLICATION NUMBER: 60/133,865
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100.0%; Pred. No. 1.
tive 0; Mismatches
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100.0%; Pred. No.
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FILING DATE: 1999-05-12
APPLICATION NUMBER: 60/133,866
FILING DATE: 1999-05-12

APPLICATION NUMBER: 60/ FILING DATE: 1999-05-12

/133,867

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128 LGGQISV 134

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                                   Query Match
Best Local Similarity
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                                                                                                                ; ORGANISM: Homo sapiens US-10-060-830-1114
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US-10-060-830-1114
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                                                                                                                                                                              SOFTWARE: Aeomica
SEQ ID NO 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 08/123,975
PRIOR FILING DATE: 1993-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PB0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gu, Yizhong
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ORGANISM: Artificial Sequence
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179 LGGQISV 185
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                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                            FILING DATE: 2001-05-23
APPLICATION NUMBER: US 60/325,062
FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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                                               Score 7; DB 9; Pred. No. 2e+
0; Mismatches
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o. 2e+02;
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o. 1.4e+02;
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                                                                                                     Query Match
Best Local (
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SEQ ID NO 47749
                                                                                  Matches
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                     PEATURE:
OTHER INFORMATION: MAP TO AL109809.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 0.88
OTHER INFORMATION: EST_HUMAN HIT: AM406955.1, EVALUE 1.00e-01
OTHER INFORMATION: SWISSPROT HIT: P01871, EVALUE 7.00e-03
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PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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111 LTYASS 116
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11 LTYASS 16
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                                                                                Local Similarity hes 6; Conserv
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FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ON NUMBER: PCT/US01/00670
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5. 3.7e+02;
                                                                                                                      Length 100
                                                                                Indels
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CURRENT APPLICATION NUMBER: US/09/949,510
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 108
TYPE: PRT
ORGANISM: Human
US-09-949-510-1
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Search completed: May 15, 2003, 13:26:35 Job time: 25.3108 secs
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US-09-949-510-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-866-20
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US-09-955-866-20
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Best Local Similarity luv.
Thes 6; Conservative
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Best Local Similarity
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CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/233,867
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
SEQ ID NO 20
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chait et al.
TITLE OF INVENTION: METHOD FOR THE COMPARATIVE QUANTITATIVE ANALYSIS OF TITLE OF INVENTION: PROTEINS AND OTHER BIOLOGICAL MATERIAL BY ISOTOPIC TITLE OF INVENTION: LABELING AND MASS SPECTROSCOPY FILE REFERENCE: Seq. List 1-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sullivan, John K.
APPLICANT: Holst, Paige
APPLICANT: Yoshinaga, Steven Kiyoshi
TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
FILE REFERENCE: 00,759-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fox, Michael
                                                                                                         191 ISRYEG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 TVPKEL 87
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6 TVPKEL 11
                                                                      111111
47 ISRYEG 52
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5. US20020107363A1
                                                                                                                                                  Conservative
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                                                                                                                                                1.4%; Score 6; DB 9; Length 108; 100.0%; Pred. No. 4e+02; Live 0; Mismatches 0; Indels
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5. 3.8e+02;
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Result
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Maximum DB
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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# ALIGNMENTS

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### 1 C; Superfamily: hexose phosphat C; Keywords: membrane protein; A; Note: this is a revision to the sequence from reference A30395 R; Friedrich, M.J.; Kadner, R.J. J. Bacteriol. 169, 3556-3563, 1987 A; Title: Nucleotide sequence of the uhp region of Escherichia coli. A; Reference number: A30395; MUID:87279903; PMID:3301805 A; Accession: C26925 A; Nolecule type: DNA A; Molecule type: DNA A; Residues: 2-440 <ISL> A; Residues: 2-440 <ISL> A; Cross-references: GB: M89479; NID: g148116; PIDN: AAA24726.1; PID: g148119 A; Cross-thic is a revision to the sequence from reference A30395 A; rule: Structure and function of the uhp genes for the sugar phosphate transport sy A; Reference number: A41853; MUID:92234930; PMID:1569007 A; Accession: G41853 Q A; Map position: 82 min C; Superfamily: hexose phosphate transport protein uhpT NAD transmembrane A;Molecule type: DNA A;Residues: 'M',87,'VCRALGAE',96,'L',98,'P',100,'L',102,'FTG',139-141,'SVNGLVFTYRA',1 A;Note: this sequence has been revised in reference A41853 C;Comment: This is one of the proteins involved in the expression of uhpT, a gene for A;Cross-references: GB:AE000444; GB:U00096; NID:g2367258; PIDN:AAC76690.1; PID:g23672 A;Experimental source: strain K-12, substrain MG1655 R;Island, M.D.; Wei, B.Y.; Kadner, R.J. A; Title: The complete genome sequence of Escherichia coli K-12 A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Accession: D65168 C;Species: Escherichia coli C;Date: 30-Jun-1991 #sequence\_revision 14-Nov-1997 #text\_change 01-Mar-2002 C;Accession: D65168; G41853; C26925; S30078 A;Gene: uhpC C; Genetics: R; Island, M.D.; Wei, B.Y.; Kac J. Bacteriol. 174, 2754-2762, A; Molecule type: DNA A; Residues: 1-440 <B Science 277, 1453-1462, 1997 R; Blattner, regulatory protein uhpC -C; Species: Escherichia co. A;Status: preliminary; nucleic acid sequence not shown; translation not shown R;Blattner, F.R.; Plunkett .A.; Rose, D.J.; Mau, B.; Query Match Best Local Matches 197 ILANGVLSR 205 1-440 <BLAT> Similarity 9; Conserv Conservative orientation Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, fau, B.; Shao, Y. 2.2%; Escherichia coli (strain K-12) sugar phosphate transport system ç Score 9; DB 1; Pred. No. 0.62; Mismatches Length 440 0, Indels 0, Gaps 0

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RESULT

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A; Title: The evolutionarily A; Reference number: A39384; A; Accession: D39384
                                                                                                     R;Bellefroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant, Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991
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C;Accession: F86050
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 A; Molecule t
A; Residues:
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A; Residues: 1-440 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulator of uhpT [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A;Title: Complete genome sequence
A;Reference number: A99629; MUID:2
A;Accession: D91204
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gasawara, N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                              finger protein HTF6 - human (fragment)
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                                                                                                                                         ;Species: Homo sapiens (man)
;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change;Accession: D39384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:AE005174; NID:g12518499; PIDN:AAG58866.1; Experimental source: strain O157:H7, substrain EDL933
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                                                                   conserved Krueppel-associated box MUID:91219421; PMID:2023909
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Shiba, T.; Hattori,
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Shinagawa,
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A; Residues: 1-163 <AAA>
 C;Accession: A39384 R;Bellefroid, E.J.;
                            finger protein HPF4 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 08-Dec-2000
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A;Title: The evolutionarily conserved Krueppel-associated box domain defines a A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Accession: E39384
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C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
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A;Title: The evolutionarily conserved Krueppel-associated box domain defines A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Accession: B39384
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C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                          A;Cross-references: GB:M61869
C;Keywords: DNA binding; zinc
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C; Date: 20-Mar-1992 #sequence
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C; Date: 27-Mar-1992 #sequence_revision
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A; Residues: 1-195 <BEL>
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                                                                                                                                                                                                                          similarity 100.0%;
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8; Conserv
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human (fragment)
                                                                                                                                                                                                                                                                          zinc
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LOO.0%; Pred. No. 2.
Lve 0; Mismatches
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 D.A.;
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Pred. No.
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Lecocq,
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Revelant,
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A;Title: The evolutionarily conserved Krueppel-associated box domain defines A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Steference A39384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AB2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein RC1290 [imported] - Rickettsia conorii (strain Malish C;Speciles: Rickettsia conorii C;Speciles: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001 C;Accession: B97861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
B97861
                                                                                                                                                A; Experimental source: C; Genetics:
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                                                                                                                               A;Gene:
                                                                                                                                                                  A;Cross-references: GB:BA000019; PIDN:BAB75860.1; A;Experimental source: strain PCC 7120
                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-264 < KUR>
                                                                                                                                                                                                                                                        A;Reference number: AB1807;
A;Accession: AB2326
                                                                                                                                                                                                                                                                                         A; Title: Complete Genomic
                                                                                                                                                                                                                                                                                                             DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                        R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
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A; Residues: 1-25!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A; Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Science 293, 2093-2098, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA A; Residues: 1-196 <BEL>
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                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein alr4161 [imported] - Nostoc sp. (strain
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Best Local :
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Best Local :
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242 ALKVELIG 249
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nes 8; Conserv
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   YVRVVPQT 364
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8; Conserv
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                                                     100.08;
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                                                         Score 8; DB 2
b; Pred. No. 4.5
0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                          M.; Yasuda,
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R; anonymous, The Xylella tast1010sa COUNSULTING OF THE XYLELLA TAST1010sa COUNSULTING OF THE SEQUENCE OF THE PLANT PATHOGEN XYLELLA fastidiosa. A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 bel
                                                                                                                          hypothetical protein XF1865 [imported] - Xylella fastidiosa C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_ch
                                                                                                                                                                               RESULT
A82629
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A; Residues: 1-624 <DIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YER147c - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change
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S50650
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Best Local Similarity
Watches 8; Conserv
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A;Map position: 19p12-19p12
C;Superfamily: zinc finger pro
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C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #te
                                                                                        C; Accession: A82629 R; anonymous, The Xylella fastidiosa Consortium of the Organization
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A; Cross-references: SGD:S0000949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Dietrich, F.S.
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A; Residues: 1-595 < PON>
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R; Poncelet, D.
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mes 8; Conserv
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Pred. No
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                                                                                                                                                                                                                                                                                                                                           .8
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#text\_change

19-Apr-2002

8229,

9115,

9132,

9981,

and

0

Indels

0

Gaps

0

Length 595;

repeat homology

PID:g1017722

ç

Indels

0;

Gaps

0

(strain

9a5c)

for Nucleotide

Seq

Length 624;

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A.Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A.Authors: Farreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.G. de Oliveira, M.C.; de Oliveira, R.C.; Banteir, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa, A.; Muthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei, M.F.; Marino, C.P.; M.A.; da Silvei, M.F.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M. S.; M.S.; M.S.; Vettore, A.L.;
                                              A; Description: The sequence A; Reference number: Z21375 A; Accession: T33602
                                                                                                                                                          C;Accession: T33602
R;Kellen, J.; Krame
                                                                                                                                                                                                      hypothetical protein E02H9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                     R;Kellen, J.; Kramer, J.; Hawkins, M. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid E02H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein B14D6.630 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: NCSP:B14D6.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.630
A;Experimental source: BAC clone B14D6; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-117 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z25022
A;Accession: T49511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: XF1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Contents: annotation
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A; Residues: 1-100 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Superfamily: Neurospora
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHLVTYQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGDLDIE 61
                        preliminary;
type: DNA
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                           translated
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100.0%; Pred. No.
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Pred. No.
                           from GB/EMBL/DDBJ
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22;
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A; Map position:
A; Introns: 89/2
Search completed: May 15, Job time: 39.7473 secs
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                                                                                                                                                                                             A; Introns: 44/3; 82/1; 102/3
                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: T34009
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y49G5A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34009
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                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-182 <BEC>
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                                                                                                                                                                                                                            A; Gene: CESP:Y49G5A.1
                                                                                                                                                                                                                                                                               A;Cross-references:
                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      R; Becker, M.; Tin-Wollam, A.M.; Yoakum, M.
Submitted to the EMBL Data Library, February 1999
N; Description: The sequence of C. elegans cosmid Y49G5A
                                                                                                                                                                                                                                                            Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                               Query Match
Best Local
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                                                                162
                                                                                               137 SKFCPAG 143
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                                                                                                                                             Госат
                                                                SKFCPAG
                                                                                                                              Similarity 7; Conserv
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Se: strain Bristol N2; clone E02H9
                                                                                                                                                                                                                                                            EMBL:AF125968; PIDN:AAD14760.1; GSPDB:GN00023; CESP:Y49G5A.1
:e: strain Bristol N2; clone Y49G5A
                                                                                                                          1.7%; Scu
100.0%; Pi
               2003, 13:25:55
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 100 seq length: 700
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Match
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                                                                                                                             US-08-111-939-22
US-08-162-402B-16
US-07-607-538C-4
US-08-162-402B-4
US-08-162-402B-4
US-08-111-939-21
US-08-111-939-25
US-08-111-939-25
US-08-111-939-25
US-08-111-939-25
US-08-114-901-24964
US-08-626-685A-10
US-08-626-685A-10
US-08-626-685A-10
US-08-162-605A-20
US-08-162-402B-13
US-08-162-402B-14
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            49-004-2
74-318-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Appl
Sequence 16, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 25, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 24, Appl
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Sequence
Sequence
Sequence
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Sequence
Sequence
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Sequence
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Sequence
    Sequence
Sequence
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10, Appl
2, Appl
503, Appl
6, Appl
11, Appl
13, Appl
14, Appl
15, Appl
17, Appl
17, Appl
17, Appl
18, Appl
18, Appl
18, Appl
2, Appl
3, Appl
46, ```

| 45                | 44                | 43                | 42                | 41                | 40                | 39                | 38                | 37                | 36              | 35                | 34                | .33               | 32                | 31                | 30                | 29                | 28                |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| 6                 | σ                 | σ                 | 6                 | σ                 | σ                 | σ                 | σ                 | σ                 | 6               | 6                 | 6                 | 0                 | 6                 | 6.                | 6                 | 6                 | 6                 |
| 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4             | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               | 1.4               |
| 227               | 221               | 221               | 219               | 218               | 218               | 214               | 209               | 208               | 202             | 202               | 202               | 202               | 202               | 202               | 202               | 202               | 202               |
| 4                 | 4                 | 4                 | 4                 | N                 | _                 | 4                 | N                 | 4                 | 4               | ω                 | ω                 | ω                 | ယ်                | N                 | N                 | N                 | N                 |
| US-08-871-572B-14 | US-09-670-141-4   | US-09-198-956-4   | US-08-934-627B-6  | US-08-162-402B-5  | US-07-607-538C-5  | US-08-861-774E-48 | US-08-248-839C-58 | US-08-961-083-214 | US-08-949-004-4 | US-08-652-446-2   | US-08-465-585C-2  | US-08-463-074B-2  | US-08-870-815-4   | US-08-754-108-2   | US-08-462-390B-2  | US-08-461-379A-2  | US-08-463-081B-2  |
| Sequence 14, Appl | Sequence 4, Appli | Sequence 4, Appli | Sequence 6, Appli | Sequence 5, Appli | Sequence 5, Appli | Sequence 48, Appl | Sequence 58, Appl | Sequence 214, App | 4               | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 4, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli |

ALIGNMENTS

RESULT 1 US-08-111-939-22

Sequence 22, Application US/08111939

Patent No. 5460951

GENERAL INFORMATION:
APPLICANT: Kawai, Shinji
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Okazaki, Makoto
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
TITLE OF INVENTION: Protein and Process for its Production
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/111,939
FILING DATE: 26-AUG-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: JP 230029/92
FILING DATE: 28-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 33,694
REGISTRATION NUMBER: 33,694
REGISTRATION NUMBER: 02481.1321-00000
TELEPHONE: 202-408-4000

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RESULT 3
US-07-607-538C-4
  밁
   뭥
   US-08-162-402B-16
   US-08-162-402B-16
   Query Match
Best Local
  Sequence 4, Application US/07607538C Patent No. 5455031
   Query Match
Best Local S
  Matches
   Sequence 16, Application US/08162402B Patent No. 5972337
   Matches
  ATTORNEY_AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
  GENERAL
   SEQUENCE CHARACTERISTICS:
   GENERAL INFORMATION:
   STRANDEDNESS:
TOPOLOGY: unk
MOLECULE TYPE:
APPLICANT:
APPLICANT:
APPLICANT:
  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
   CORRESPONDENCE ADDRESS
  TITLE OF INVENTION:
  129 PPIVARY 135
  351 PPIVARY 357
  APPLICANT:
   351 PPIVARY 357
  TUMBER OF SEQUENCES:
  STREET: 444 South
CITY: Los Angeles
STATE: CA
  Local Similarity les 7; Conserv
   APPLICATION NUMBER: US/08/162,402B FILING DATE: 03-DEC-1993
   COUNTRY: U
   88 PPIVARY 94
   Local Similarity
  TELEX:
  TELEFAX:
   APPLICATION NUMBER:
   LENGTH:
   ADDRESSEE:
  No.
  INFORMATION:
  amino acid
   159 amino acids
   E: Pretty, Schroeder & Poplawski 444 South Flower St., 19th Floor
  213-489-4210
  USA
  LAROCCA, DAVID J.

VENTION: 46 KDALTON HUMAN MILK FAT
VENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
                      Ceriani Dr., Roberto L.
  PETERSON, JERRY A.
  Conservative
  Conservative
  CERIANI, ROBERTO L.
             Peterson
   unknown
   IBM Compatible
   Diskette
   unknown
  1.7%;
   1.7%;
100.0%;
   16:
 Jerry A.
d J.
   b; Score 7; DB 2
b; Pred. No. 37;
0; Mismatches
  Score 7; DB 1
; Pred. No. 28;
0; Mismatches
  DB 1;
  0;
   Length 159;
  Length 115;
  Indels
  Indels
   0;
  0
  Gaps
   0
  0
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   ş
  ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-07-607-538C-4
  US-08-162-402B-4
   Query Match
Best Local S
Matches 7
  Sequence 4, Application US/08162402B Patent No. 5972337
  Patent No.
   GENERAL INFORMATION:
  TELEFAX: (510) 943-110
TELEX: N.A.
INFORMATION FOR SEQ ID NO:
  APPLICANT: CERIANI, ....APPLICANT: PETERSON, JERRY A.
APPLICANT: LAROCCA, DAVID J.
TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAI
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FI
TITLE OF GROUENCES: 29
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
  SOFTWARE: PatentIn Release #1.0, VGURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/607,538C
FILING DATE: 01-NOV-1990
CLASSIFICATION: 435
CLASSIFICATION: 435
   NAME: Viviana Amzel
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
  SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acid
   ATTORNEY/AGENT INFORMATION: NAME: Viviana Amzel
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
  TITLE OF
   TITLE OF
  TITLE OF
   TITLE OF
  351 PPIVARY 357
   TITLE OF INVENTION:
   ALUKESSEE: V. Amzel & Assoc.
STREET: 2055 No. 5455031th Broadway
CITY: Walnut Creek
STATE: California
COUNTED. TO
   STREET: 444 South
CITY: Los Angeles
STATE: CA
COMPUTER: IBM COLOPERATING SYSTEM:
   ZIP: 90071
   COUNTRY:
   TOPOLOGY:
  STRANDEDNESS:
   TELEPHONE:
  OPERATING SYSTEM:
   COUNTRY:
  ADDRESSEE:
  OF INVENTION:
   7; Conserv
  94596
   amino acid
  INVENTION:
   CA
   INVENTION:
   E: Pretty, Schroeder 444 South Flower St.,
  USA
  218 amino acids
  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS 5.0
Patentin Release #1.0, Version #1.25
  Conservative
IBM Compatible SYSTEM: DOS
   linear
   (510)
                                 Diskette
  protein
   single
  943-1189
   1.7%; Score 7; DB 100.0%; Pred. No. 50 tive 0; Mismatches
  FUSION PROTEIN, POLYMINITERATION STECIFITY
   POLYPEPTIDE WITH 46
DIFFERENTIATION ANTIGEN BINDING SPECIFITY AND CLOTTING
   USE THEREOF
   NUCLEOTIDE
   Schroeder & Poplawski
Flower St., 19th Floor
  4..
  CRFCC-004
   PROTEIN,
  DB 1;
   POLYNUCLEOTIDE AND
   FRAGMENTS & FUSION PROTEIN
   Length 218;
   0
   POLYRIBO-
   Gaps
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RESULT 5
US-08-492-027A-4
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   Ş
  US-08-162-402B-4
   Sequence 4, Application US/08492027A Patent No. 5912333
   Matches
  Query Match
  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  GENERAL INFORMATION:
  ATTORNEY_AGENT INFORMATION:

NAME: AMZEL, VIVIANA

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: P66

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213-622-7700
  INFORMATION FOR SEQ ID NO:
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULTPH JT, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 01
   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
  TELECOMMUNICATION INFORMATION:
  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  SEQUENCE CHARACTERISTICS:
   CORRESPONDENCE ADDRESS:
   APPLICANT:
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
   NUMBER OF SEQUENCES:
   MOLECULE TYPE: peptide
  351 PPIVARY 357
   TLE OF INVENTION:
                 TOPOLOGY:
   TELEPHONE:
  FILING DATE: .
   COUNTRY:
  28 PPIVARY 34
  APPLICATION NUMBER:
   TOPOLOGY:
  STRANDEDNESS:
   TELEFAX: 213-489-4210
  LENGTH:
   ADDRESSEE:
  Local Similarity 100 es 7; Conservative
  LENGTH:
   APPLICATION NUMBER:
  APPLICATION NUMBER:
   22040-0747
  Falls Church
  APPLICATION DATA:
                            amino acid
   amino acid
TYPE:
  P.O.
   272 amino acids
  218 amino acids
   USA
   (703)
   Burnell,
  Suzuki,
   Birch, Ste
.0. Box 747
  unknown
   FastSEQ for Windows Version 2.0
  (703) 205-8000
 protein
  03-DEC-1993
   unknown
   205-8050
  Shoichi
  DNA Encoding Carbonic Anhydrase
  1.7%; Score 7;
100.0%; Pred. No
tive 0; Mismat
   Stewart,
   James N
  US/08/492,027A
  US/08/162,402B
  4.
  4.
   P66
  0760-206
   Kolasch and Birch
  mismatches
  38215
   Length 218;
  0; Indels
  0
  Gaps
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Query Match
Best Local Similarity
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US-09-304-799-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-304-799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-111-939-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 108
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, April
Sequence 1, April
5 No. 6391649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/304,799 CURRENT FILING DATE: 1999-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Rockefeller University
TITLE OF INVENTION: MATERIAL BY ISOTOPIC LABELING AND MASS SPECTROSCOPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 1119-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                           FILING DATE: 03-DEC-1992 PRIOR APPLICATION DATA:
                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Bone-Related Carboxy TITLE OF INVENTION: Protein and Process NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 ISRYEG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 ALKVELI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 ALKVELI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 ISRYEG
                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 26-AUG-1993
                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                           COUNTRY:
                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                 20005-3315
                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08111939
                                                                                                                                                                                                                                                                                      3: Dunner
1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                Takeshita, Sunao
Okazaki, Makoto
Amann, Egon
                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawai, Shinji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                      Finnegan, Henderson, Farabow, Garrett &
28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1:7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%;
                                                                                                                                                                                                                                                                                                                                                                   Bone-Related Carboxypeptidase-Like Protein and Process for its Product
                                                                                                                      US/08/111,939
              JP 230029/92
                                                           JP 324033/92
                                                                                                                                                                                                                                                                                                                                                                                                                                Sunao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 2; Pred. No. 62; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6e+02;
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                                                                                                                                                                                                                                                                                                                                                                    Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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US-08-111-939-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/08111939 Patent No. 5460951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                           TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acid
                                                                                                              REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                               APPLICATION NUMBER: JP 230029/92 FILING DATE: 28-AUG-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 324033/92 FILING DATE: 03-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 KVFQGN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TILE OF INVENTION: Bone-Related Carboxypeptidase-Like INVENTION: Protein and Process for its Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
TYPE: amino acid
TOPOLOGY
                                                                                                                                                                NAME: Forman, David S. REGISTRATION NUMBER: 33,694
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01 FILING DATE: 26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 KVFQGN 69
               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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                             amino acid
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1300 I Street, N.W.
                                               109 amino acids
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                       TELEFAX: 202-408-4000
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3315
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 324033/92
FILING DATE: 03-DEC-1992
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
                                                                                                                                                                                                                                    TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                        FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like TITLE OF INVENTION: Protein and Process for its Production NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                           279 WLEIDL 284
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ADDRESSEE: Dunner
ADDRESSEE: Dunner
1300 I Street, N.W.
12 WLEIDL 17
                                                                                                                                                                                                                                                                               NAME: Forman, David S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 26-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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Takeshita, Sunao
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100.0%; Pr
                                                       1.4%; Score 6; DB
100.0%; Pred. No. 2.
tive 0; Mismatches
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Pred. No.
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                                                                      DB 1; Le
5. 2.7e+02;
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o. 2.7e+02;
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; Sequence 4964, Application US/09134001C ; Patent No. 6380370

RESULT 10 US-09-134-001C-4964

Length 123;

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RESULT 11
US-08-626-685A-10
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4964
LENGTH: 115
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Best Local Similarity
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                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Smith, Kelli E.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Weinshank, Richard L.
APPLICANT: Linemeyer, David
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
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                     TOPOLOGY:
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                                                        LENGTH:
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E: New York
TRY: U.S.A.
10036
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5972624
                                amino acid
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1185 Avenue of the Americas
                                                      123 amino acids
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212-391-0525
protein
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Matches 6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                         TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                           235 ASSSWQ 240
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nes 6; Conserv
22 ASSSWQ
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                               NAME: POREMBSKI, PRISCILLA E. REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                 amino acid
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100 ABBOTT PARK ROAD
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                                                        Conservative
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SHERI L. BUIJK
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100.0%; Pred. No. 3e
Live 0; Mismatches
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                                                                   Score 6; ; Pred. No.
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RESULT 13 US-08-054-480-2

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RESULT 14
US-09-149-476-503
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Best Local
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                                                                                                                                                                                                                                                                            Patent No.
                                                               EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 00/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                        ENERAL INFORMATION:
APPLICANT: Rosen et
                                                                                                                                                                                                          FILE REFERENCE: P2002P1
                                       BARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 146 amino acids
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: MILLEN, WHITE, ZELANO, STREET: 2200 CLARENDON BOULEVARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goebel, Werner
APPLICANT: Libby, Stephen
APPLICANT: Heffron, Fred
TITLE OF INVENTION: CYTOLYSIN GENE AND GENE PRODUCT
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| 0TCASD 86
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
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R FILING DATE: 1997-04-11
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R APPLICATION NUMBER: 60/047,612
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 APPLICATION NUMBER: 60/047,600 FILING DATE: 1997-05-23 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,503 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,615 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-03-07 APPLICATION NUMBER: FILING DATE: 1997-03 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/0 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/0 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,618 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,617 FILING DATE: 1997-05-23 APPLICATION NUMBER: FILING DATE: 1997-05 APPLICATION NUMBER: 60/047,502 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: APPLICATION NUMBER: 60/040,334 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/043,569 APPLICATION NUMBER: 60/047,596 APPLICATION NUMBER: APPLICATION NUMBER: 60/047,582 PPLICATION NUMBER: 60/043,314 ILING DATE: 1997-04-11 ILING DATE: 1997-05-23 1997-05-23 1997-03-07 60/043,580 60/047,613 60/047,583 60/047,597 60/047,598 60/047,583 60/040,163 60/040,336

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MEDIUM TYPE: Diskette,
COMPUTER: IBM Compatib
OPERATING SYSTEM: MS-D
                                      FILING DATE: NO. 592 PRIOR APPLICATION DATA:
                                                                                                                    SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
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NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET 12,389
REFERENCE/DOCKET NUMBER: F-5230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)985-2340
TELEPHONE: (212)985-2340
TELEPHONE: (212)985-234

INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 annion acids
TYPE: annion acids
TYPE: annion acids
TYPE: annion acids
TYPE: protein
TOPOLOGY: linear
MOLECULE TYPE: protein
TRAMENUT TYPE: intermediate fragment
ORIGINAL SOURCE:
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seq length: 700

    protein search, using sw model

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418
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P09836 escherichia
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Q9w6r5 fugu rubrip
P05046 glycine max
Q44539 haemophilus
Q18090 caenorhabdi
P58588 listeria in
Q1009 schizosacch
P07173 rhodopseudo
Q54873 cricetulus
Q59586 mycobacteri
P49163 arabidopsis
P57877 pasteurella
Q404804 pseudomonas
P38658 schistosoma
Q00612 mus musculu
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P05370 rattus norv
Q40308 saccharomyc
Q04451 bombyx mori
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| JI ST<br>176728;<br>1982 (Rel.)<br>1992 (Rel.)<br>1992 (Rel.)<br>1992 (Rel.)<br>1992 (Rel.)<br>1992 (Rel.)<br>1992 (Rel.)<br>1993;<br>101. 169<br>101. 169<br>101. 169<br>101. 169<br>101. 169<br>101. 175<br>101. 174<br>101. 175<br>101. 174<br>101. 175<br>101. 175                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                              |
| II STANDAI P76728; 9389 (Rel. 10, 992 (Rel. 40, 001 (Rel.  | 44444444                                                                                                                                                     |
| STANDARD;  16728; 19 (Rel. 10, Cre 12 (Rel. 27, Las 1667. a coli. protein uhpc. a coli. proteobacteria; be sequence of tol. 169:3556-35  AUG-1990) to tol. 169:3556-35  AUG-1990) to tol. 174:2754-27  ROM N.A. AUG-1990) to tol. 175:51-561(1993)  OLE. D. Plunkett G. D. P | 109<br>110<br>1110<br>1114<br>1125<br>129<br>130<br>130<br>130<br>130                                                                                        |
| STANDARD; PRT; (Rel. 10, Created) (Rel. 23, Last sequency (Rel. 23, Last sequency (Rel. 40, Last annotat. Protein uhpC. 67. coli. roteobacteria; gamma sul 562;  Sequence of the uhp re 1. 169:3556-3563(1987). MALA MARA MARA MARA MARA MARA MARA MARA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                              |
| pRT; sequence u annotation annota | RLA5<br>RLA5<br>RLA3<br>RSMB<br>YG4U<br>HPAA<br>CY52<br>CCKN<br>RSB J<br>RSB J<br>PEME                                                                       |
| PRT; 4 ed) sequence up sequence up annotation (1985; ; ; ; ; uhp region (1987).  EMBL/GenBa EMBL/Ge | RLA5_SCHPO KDGF_ERWCH RLA3_SCHPO MSMB_MACMU YG44U_YEAST HPAA_HELAC CY52_SCHPO CCKN_METIG RS8_METIJA RS8_METIL PEMK_ECOLI                                     |
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| ** ** ** ** ** ** ** ** ** ** ** ** **                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                              |

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Best Local S
Matches
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TRANSMEM
                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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01-JUN-1994
16-OCT-2001
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InterPro; IPR003662; sub_transporter.
Pfam; PF0083; sugar_tr; 1.
TIGRFAMS; TIGR00881; 2A0104; 1.
PROSITE; PS00942; GLPT; 1.
                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                   -1- SUBCELLULAR LOCATION: Nuclear (Probable).
-1- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING EMBRYONIC DEVELOPMENT.
-1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                      "The evolutionarily conserved Kruppel-associated box domain subfamily of eukaryotic multifingered proteins."; proc. Natl. Acad. Sci. U.S.A. 88:3608-3612(1991).
-i- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.
                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                Bellefroid E.J.,
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-91219421;
                                                                                                                                                                                                                                                                                                                                                                                  ZN90_HUMAN
Q03938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport;
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PIR; G41853; RCECTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M17102; AAA24722.1; ALT_INIT.
EMBL; M89479; AAA24726.1; -.
EMBL; M61870;
                                                                                                                - ! - SIMILARITY: CONTAINS 1 KRAB DOMAIN
                                                                                                                                                                                                                       Martial J.A.;
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                      European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                             FINGER PROTEINS.
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9; Conser
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(Rel.
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llarity 100.0%; Pred. No. 0.31;
Conservative 0; Mismatches
AAA36028.1;
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Poncelet D.A., L
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O (Zinc finger protein H
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                                                  There are no resu
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ZN_FING
ZN_FING
NON_TER
                                                                                                                                                                                                                             Mao M., Fu G., Wu J.-S., Zhang Q.-H
He K.-L., Gu B.-W., Han Z.-G., Shen
Wang Y.-X., Chen S.-J., Chen Z.;
"Identification of genes expressed
stem/progenitor cells by expressed s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM0034; KRAB; 1.
SMART; SM00355; Znf_C2H2;
PROSITE; PS50805; KRAB; 1
PROSITE; PS00028; ZINC_FII
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                              J. Biol. Chem. 274:35741-35748(1999).
-I- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR
-I- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                     Han
                                                                                                                                                                                                                                                                                     TISSUE-Blood;
MEDLINE-98318631;
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                            ZNF254 OR BMZF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00096; zf-C2H2; Pfam; PF01352; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
                                                                                                                                                                            MEDLINE=20054457;
                                                                                                                                                                                     SEQUENCE FROM N.A.
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Nuclear protein
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InterPro; IPR000822; Znf_(
                                                                                                                    domain KRNB.";
                                                                                                                            Han Z.-G., Zhang Q.-H., Ye M., Kan L.-X., Gu B.-W., He K.-L., Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., Chen Z.; "Molecular cloning of six novel Kruppel-like zinc finger genes from the matopoietic cells and identification of a novel transregulatory
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
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                                                  SIMILARITY: CONTAINS 1 KRAB DOMAIN
                                                                        SIMILARITY: BELONGS
                                                               FINGER PROTEINS.
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Natl. Acad. Sci. U.S.A.
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HGNC:13165; Z
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PS00028; ZINC_FINGER_C2H2_1;
PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Creatt,
(Rel. 40, Last sequence update)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
: protein 254 (Bone marrow zinc finger
stic cell derived zinc finger protein )
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173
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Primates;
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100.0%; Pr
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Pred. No.
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C2H2-TYPE
C2H2-TYPE.
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                                                                                                                                                                                                          95:8175-8180(1998).
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Yu Y.-P.,
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Xu S.-H.,
                    a collaboration -
MBL outstation -
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RESULT 4
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ZNF117
Homo sapiens (Human).
Homo sapiens (Human).
Homota; Metazoa; Chordata;
Thoria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                              SEQUENCE OF 1-166 FROM N.A. MEDLINE-91219421; Pubmed-2023909;
                                                                                                                        "The human genome contains hundreds proteins of the Kruppel type."; DNA 8:377-387(1989).
                                                                                                                                                  TISSUE-Placenta;
MEDLINE-89377476; PubMed-2505992;
Bellefroid E.J., Lecocq P.J., Benhida
Belayew A., Martial J.A.;
                                                                                                                                                                                                                                           Zinc finger
ZNF117.
                                                                                                                                                                                                                                                                                                         HOMAN
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.

Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
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PRINTS; PR00048; ZINCFINGER.
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16-0CT-2001
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Q03924;
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                                                                                     Bellefroid E.J., Poncelet D.A.,
                                                                                                                                                                                       SEQUENCE OF 4-418 FROM
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SM00349; KRAB; 1.
SM00355; znF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NF054180; AAC39913.1;
HGNC:13047; ZNF254.
                                                                                                                                                                                                                                                                                                                                                                             h 1.9%; S
Similarity 100.0%;
8; Conservative 0;
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(Rel. 40, Last annotation
protein 117 (Zinc finger p
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1 KRAB DOMAIN.
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0; Mismatches
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ZINC FINGE
C2H2-TYPE
C2H2-TYPE
C2H2-TYPE.
C2H2-TYPE.
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                                                                                     Lecocq P.J.,
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OF C2H2-TYPE
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RESULT
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Matches 8
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InterPro; IPR000822; 2nf_C2H2.
Pfam; PP00096; zf-C2H2; 10.
ProDom; PD000003; Znf_C2H2; 5.
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 10.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
Transcription regulation; Zinc-finger; DN
                                                                                             Zinc finger protein 2
ZNF257 OR BMZF4.
Homo sapiens
                                                                                                                                                                                              _HUMAN
TISSUE-Bone marrow;
MEDLINE-20054457; PubMed-10585455;
Han Z.-G., Zhang Q.-H., Ye M., Kan
Shi S.-L., Zhou J., Fu G., Mao M.,
"Molecular cloning of six novel Kru
                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
SEQUENCE
                                                        SEQUENCE FROM N.A.
                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                         16-OCT-2001
16-OCT-2001
15-JUN-2002
                                                                                                                                                                         2257_HUMAN
Q9Y2Q1;
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ZN_FING
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HSSP; P03001; 1TF6.
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                                                                            NCBI_TaxID=9606;
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M61867; AAA58666.1; -.
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an email to license@isb-sib.ch).
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(Rel. 40, Last sequence up
(Rel. 41, Last annotation
protein 257 (Bone marrow 2
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Y -> RH (IN REF. 2).
CDB554CB69EB0B69 CRC64;
  Kan L.-X., Gu B.-W
M., Chen S.-J., Yu
Kruppel-like zinc
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ion update)
ow zinc finger
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15-JUN-2002 (Rel. /
15-JUN-2002 (Rel. /
15-JUN-2002 (Rel. /
Hypothetical zinc /
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HUMAN
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ZN_FING
ZN_FING
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 12.
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J. Biol. Chem. 274:35741-35748(1999).
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PRODOMOOO3; Znf_C2H2; 9
SMART; SM00349; KRAB; 1
SMART; SM00355; ZnF_C2H2; 10.
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-i- SUBCELLULAR LOCATION: Nuclear (Probable).
-i- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                              Homo sapiens (Human)
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    Last sequence update)
    Last annotation update)
    finger protein KIAA1473 (Fragment).

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01-JUN-1994
01-OCT-1996
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Nagase T., Kikuno R., Ishikawa A. 17, ....
"Prediction of the coding sequences of unidentified human years."

"Prediction of the coding sequences of unidentified human years."

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PRODOM; PD000003; Znf_C2H2; 2
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-sentities.
                       16-OCT-2001
Zinc finger
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical Zinc-finger;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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InterPro; IPR000822; Znf_C
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PS00028; ZINC_FINGER_C2H2_1; 12.
PS50157; ZINC_FINGER_C2H2_2; 13.
:ical protein; Transcription regulation; DNA-binding; iger; Metal-binding; Nuclear protein; Repeat.
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1. 34, Last sequence update,
1. 40, Last annotation update)
)tein 85 (Zinc finger protein HP)
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5. 4.3;
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InterPro; IPR001909; KRAB.
InterPro; IPR001822; Znf_C2H2.
Pfam; PP00096; Zf_C2H2; 15.
Pfam; PF01352; KRAB; 1.
PRINTS; PR00048; ZINCFINGER.
PRODOM; PD000003; Znf_C2H2; 13.
SMART; SM00349; KRAB; 1.
SMART; SM00355; Znf_C2H2; 15.
                                                                                                                                                                                                                                                                                                                         EMBL; U35376; AAA79179.1; -
EMBL; M61866; AAA52689.1; -
EMBL; M61868; AAA58671.1; -
PIR; A39384; A39384.
PIR; C39384; C39384.
HSSP; P08048; 7ZNF.
TRANSFAC; T04990; -
ZN_FING
                                                                                                                                                   PROSITE; PS50805; KRAB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional analysis of ZNF85 KRAB zinc the highly homologous ZNF91 family."; DNA Cell Biol. 17:931-943(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily of eukaryotic multifingered proteins.*;
Proc. Natl. Acad. Sci. U.S.A. 88:3608-3612(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: TRANSCRIPTIONAL REPRESSOR.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN
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                                                                                                                                             Repressor.
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Lecocq P.J., C
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RESULT 8
YEX7_YEAST
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01-FEB-1995 (Rel. 3.
16-OCT-2001 (Rel. 40
Hypothetical 72.1 kD
YER147C.
                                                                                                                                                        EMBL; U18917; AAB64674.1; -. SGD; S0000949; YER147C. InterPro; IPRO00873; AMP-bind. PROSITE; PS00455; AMP_BINDING; 1
Hypothetical protein; Ligase. SEQUENCE 624 AA; 72140 MW; 1
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclaromycetales; Saccharomycetaceae; Saccharomyces
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Dietrich F.S., Mulligan J.T.,
                                                                                                                                                                                                                                                                                                                                                                             entities requires a
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P40090;
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  368 RIALKVEL
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                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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8; Conserv
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T., Carpenter J., Chen
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Boriss R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Dandel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Dandel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Koetter P., Koningstein G., Kroph S., Kumano M.,
RA Kurita K., Lapidus A., Lardnois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardnois S., Lauber J., Lazarevic V.,
RA Kurita N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Schleich S., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Soldo B.,
RA Noshida K., Voshikawa H., Vannier F., Vassarotti A.,
RA Vashida K., Voshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
Poshikawa H., Danchin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adder E., Barak I., Stragier P.;

"Bacillus subtilis locus encoding a killer protein and if

"Bacteriol. 183:3574-3581(2001).

"I- FUNCTION: Has a negative effect on sporulation. It is

synthesized during vegetative growth in the absence of the synthesized during the synthes
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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"Sequence of the
                                               EMBL; AJ002571; CAA05563.1; -. EMBL; Z99110; CAB13140.1; -.
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NCBI_TaxID=1423;
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034853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98044033;
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15-JUN-2002 (Rel.
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        BG12677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshikawa H.F.,
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ce of the Gram-positive bacterium
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01-FEB-1995
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Pfam; PF00138; lectin_legA; Pfam; PF00139; lectin_legB; Pr0Dom; PD000671; Lectin_legProDom; PD000711; Lectin_leg
                                                                          EMBL; L11745; AAA33675.1;
EMBL; M25072; AAA33681.1;
PIR; A44975; A44975.
                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       "A developmentally regulated bud specific transcript sequence similarity to seed lectins."; Plant Physiol. 89:833-838(1989).
                                                                                                                                                                                                                                                                                     STRAIN-cv. Alaska;
Dobres M.S., Thompson W.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum
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                                            InterPro; IPR000985; Lectin_legA.
InterPro; IPR001220; Lectin_legB.
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SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
                                                                                                                                                                                                                                  SUBUNIT: MONOMER.
TISSUE SPECIFICITY: MOST HIGHLY EXPRESSED
                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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IS DECREASED BY MAGNITUDE).
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CARBOHYD
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PROSITE; PS01286; FA58C_2; FALSE_NEG
                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                   "Genomic structure and comparative analysis of nine conservation of synteny with human chromosome Xp22.2 Genome Res. 9:437-448(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
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                                              SEQUENCE
                                                                                         SIGNAL
                                                                                                   Cell adhesion;
                                                                                                                                                                                            EMBL;
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Kalscheuer V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W6R5;
30-MAY-2000
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                                                                   DOMAIN
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                                                                                                                                                                      InterPro; IPR000421; FA58_C.
                                                                                                                                                                                   HSSP; P12259; 1CZT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fugu rubripes (Japanese pufferfish)
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Local Similarity nes 7; Conserv
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                                                                                                                                                                                                                                                           ween the Swiss Institute of Bioinfo
                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted (By similarity). SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
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                                                                                                                                                                                                                                                                                                                                         FUNCTION: MAY BE ACTIVE IN CELL ADHESION PROCESSES
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LECTIN_LEGUME_ALPHA; FALSE_NEG.

bultigene family; Manganese; Calcium; Glycoprotein.

OR 23 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10330123;
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                                                                  X-LINKED JUVENILE RETINOSCHISIS PROTEIN F5/8 TYPE C.
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5. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                Schulz U.,
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xp22.2-p22.1.";
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                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                                                                                        a collaboration -
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"cA lectin gene insertion
"cA lectin gene insertion
"cangosable element.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dessen A., Gupta D., Sabesan S., Brewer C.F., Sacchettini J.C.; "x-ray crystal structure of the soybean agglutinin cross-linked a biantennary analog of the blood group I carbohydrate antigen." Biochemistry 34:4933-4942(1995).
                                                           ProDom; PD000671; Lectin_legA; 1.
ProDom; PD000711; Lectin_legB; 1.
PROSITE; PS00307; LECTIN_LEGUME_BETA;
PROSITE; PS00308; LECTIN_LEGUME_ALPHA;
Lectin; Glycoprotein; Signal; 3D-struc
                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send-an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=84026469; PubMed=6313203;
MEDLINE=84026469; PubMed=6313203;
Rhodes P.R., Goldberg R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
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13-AUG-1987
    CARBOHYD
                                                                                                                                                                      InterPro; IPR000985; Lectin_legA.
InterPro; IPR001220; Lectin_legB.
Pfam; PF00138; Lectin_legA; 1.
Pfam; PF00139; lectin_legB; 1.
                                                                                                                                                                                                                                                                                                                                                                EMBL; K00821; AAA33983.1; PIR; S27365; S27365.
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Biochemistry 36:15073-15080(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transposable element.";
Cell 34:1023-1031(1983).
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                                              SIGNAL
                                                                                                                                                                                                                                                                              PDB; 1SBE; 22-APR-98
PDB; 1SBF; 22-APR-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98060759; PubMed=9398234;
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1SBD; 22-APR-98.
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(Rel.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  core eudicots; Rosida; Phaseoleae; Glycine.
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                                                                                                                                                                                                                                                                                                                                                                                         Rd.";
Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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P44539;
01-NOV-1995
                                                                      Lyase; Co
                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria;
Haemophilus.
                                                                                                                                                                                                     EMBL; U32700; AAC21814.1;
HSSP; P06995; 1NAL.
TIGR; HI0142; -.
                                                                                            TIGRFAMs; TIGRO0683; nanA; 1. proSITE; PS00665; DHDPS_1; 1. proSITE; PS00666; DHDPS_2; 1.
                                                                                                                                                              InterPro; IPR002220; DHDPS.
InterPro; IPR005264; Nana.
Pfam; PF00701; DHDPS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                     PRINTS; PRO0146; DHPICSNTHASE. ProDom; PD001859; DHDPS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
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MEDLINE-95350630; PubMed-7542800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
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15-JUN-2002 (Rel. 41, Last annotation updat
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                   Local
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SUBUNIT: HOMOTRIMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE DHDPS FAMILY.
                                                                      Complete proteome. TE 164 164
     7; Conserv
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7; Conserv
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b; Pred. No. 26;
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Pred. No
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                 DB 1;
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Q18090;
16-OCT-2001
                                                                                                                                                               15-JUN-2002
15-JUN-2002
15-JUN-2002
 Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T. Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
                                      SEQUENCE FROM N.A.
STRAIN-EGD-e / Serovar 1/2a;
MEDLINE-21537279; PubMed-11679669;
                                                                                                                                                                                                                               LISMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases i- FUNCTION: ESSENTIAL FOR THE IMPORT OF PROFEIN PRECUMITOCHONDRIA (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Integral membrane protein. Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable mitochondrial import receptor submit
                                                                                                         Listeria monocytogenes.
Bacteria; Firmicutes; F
                                                                                                                                                                                                        P58588;
                                                                                                                                                                                                                    Y073_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                             NCBI_TaxID=1639;
                                                                                                                                                 Hypotheticl
                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transport; Protein transport; Outer
Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z70034; CAA93850.1; WormPep; C18E9.6; CE05298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE TOM40 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sims M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                   180 GGQISVL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
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|||||||
3 EGILANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer membrane (By similarity)
                                                                                                                                                                                                                                                                                    GGQISVL 187
                                                                                                                                                                                                                   LISMO
                                                                                                                                                                                                                                                                                                                                    l Similarity
7; Conserv
                                                                                                                                                (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
protein Lmo2473.
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                                                                                                                                                                                                                                                                                                                                                  1.7%;
                                                                                                            Bacillales;
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                                                                                                           Listeriaceae;
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5. 27;
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Search completed: May 15, 2003, 13:23:05 Job time : 16.4678 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.D., Fishi H., Portillo F.G., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.M., Kaerst U., Kreft J., Ruhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Vicente J.M., Ng E., Nedjari H., Nordsiek G., Movella S., de Pablos B., Perez-Diaz J.C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.A., Voss H., Wehland J., Cossart P.; "Comparative genomics of Listeria species."; Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     82 TVPKELL 88
|||||||
258 TVPKELL 264
                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome. SEQUENCE 322 AA; 34973 MW; 50180FCBADF63A31 CRC64;
                                                                                                                                                                                                                                                                                                                           EMBL; AL591983; CAD00551.1; -. Listilist; LMO02473; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: BELONGS TO THE UPF0052 FAMILY.
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
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1 EELGDGCGHIVTSQDSGTMT.....
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1305.856 Million cell updates/sec
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#### SUMMARIES

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| 12.8<br>12.8<br>12.8<br>9.1<br>9.1<br>3.7<br>3.7<br>3.7<br>3.7                                                                                                                                  | Query<br>Match        |
| 487<br>539<br>586<br>398<br>398<br>101<br>101<br>101<br>109                                                                                                                                     | Query Match Length DB |
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| AAU00628<br>AAU00630<br>AAU00629<br>AAE22715<br>AAU79459<br>AAU19467<br>ABP51369<br>ABP51461<br>AAM38946                                                                                        | ID:                   |
| H H H H H H H H H H H H H H H H H H H                                                                                                                                                           | Des                   |
| Novel<br>Novel<br>Novel<br>Human<br>Human<br>Human<br>Human<br>Human                                                                                                                            | Description           |
| Novel human protei<br>Novel human protei<br>Novel human protei<br>Human neuropilin-H<br>Human Neuropilin-H<br>Human diagnostic a<br>Human MDDT SEQ ID<br>Human MDDT SEQ ID<br>Human polypeptide | tion                  |

| 45                 | 44       | 43                 | 42       | 41                 | 40                 | 39                 | 38                 | 37                 | 36                 | 35       | 34       | 33       | . 32               | 31                 | 30       | 29                | 28       |                    | 26                 | 25                 | 24                 | 23       | 22       | 21       | 20       | 19       | 18       | 17                 | 16       | 15       | 14       | 13        | 12       | 11                 |
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| 641                | 639      | 610                | 524      | 523                | 474                | 474                | 464                | 430                | 414                | 385      | 359      | 350      | 350                | 350                | 350      | 312               | 297      | 275                | 263                | 220                | 217                | 206      | 204      | 126      | 115      | 694      | 493      | 364                | 353      | 273      | 193      | 128       | 117      | 117                |
| 22                 | 22       | 22                 | 21       | 18                 | 22                 | 22                 | 22                 | 23                 | 22                 | 22       | 20       | 22       | 22                 | 22                 | 21       | 22                | 22       | 22                 | 15                 | 22                 | 23                 | 21       | 23       | 22       | 22       | 21       | 22       | 22                 | 20       | 23       | 22       | 22        | 23       | 22                 |
| ABB58034           | ABG17654 | AAU34821           | AAB28588 | AAW38187           | ABB66823           | ABB62780           | AAM93631           | ABP28277           | AAE10702           | AAG81097 | AAW81359 | AAB94884 | AAB93281           | AAM93217           | AAB12145 | AAU14605          | ABG12597 | AAB86528           | AAR63754           | ABG21553           | ABP26698           | AAY96283 | AAM48377 | AAM90976 | ABG27684 | AAY99661 | ABG16286 | AAB94710           | AAY39779 | ABG60044 | AAM40732 | AAM79595  | ABP51401 | AAB92967           |
| Drosophila melanog | -        | E. coli cellular p |          | Arabidopsis SCAREC | Drosophila melanog | Drosophila melanog | Human polypeptide, | Streptococcus poly | Mouse GM3 synthase |          | alpha-2- |          | Human protein sequ | Human polypeptide, | ō        | Novel bone marrow |          | P. pantotrophus GB | New flower bud ind | Novel human diagno | Streptococcus poly |          | _        | 5        |          | 5        |          | Human protein sequ | Ü        |          |          | protein s | MDDT SEC | Human protein sequ |

# ALIGNMENTS

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RESULT 1
AAB19126
ID AAB1
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AC AAB1
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KW Lymp
KW Inmou
KW Inmou
KW Card
XX Card
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YX WO20
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                                                                                                                                                                                                                                                                   AAB19126;
                                                                                                                                                                                                                                                                                     AAB19126 standard; Protein; 503 AA.
                                                                                                                                                                                                                             Polypeptide isolated from lymph node stromal cells of fsn -/-
                                                                                                                                                                                                                                              19-FEB-2001 (first entry)
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mice.

Lymph node stromal cell; fsn -/- mice; inflammatory disorder; immune system disorder; cancer; viral disorder; HIV infection; blood vessel growth; tumour necrosis factor disorder; arthritis; inflammatory bowel disease; fibroblast growth factor-mediated disorder; cardiac failure.

Mus sp.

WO200058463-A1.

05-OCT-2000.

18-FEB-2000; 2000WO-NZ00015

25-MAR-1999; 26-AUG-1999; 99US-0276268 99US-0383586

(GENE-) GENESIS RES & DEV CORP LTD.

Strachan L, Murison JG; Sleeman ŗ Abernethy N, Onrust Kumble

WPI; 2000-664924/64.

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RESULT 2
AAU00628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from arthritis, inflammatory bowel disease and cardiac failure and a fibroblast growth factor-mediated disorder. It is also useful in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, to quantify levels of protein or cognate corresponding ligand or receptors, as antiinflammatory agents, and in compositions for the treatment of skin, connective tissue and immune system diseases. The polynucleotide is useful as marker for tissue, as a chromosome marker or tags in the identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides and their polypeptides are useful for treating an inflammatory disorder, disorder of immune system and cancer selected from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a viral disorder, in particular HIV infection and for modulating the growth of blood vessels. The polypeptides are useful for treating a tumour necrosis factor (TNF) mediated disorder, such as those selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide expressed in mammalian fsn -/- lymph node stromal cells, useful for modulating growth of blood cells, for treating inflammatory and tumour necrosis factor-mediated disorders, cancer and viral disorders
                                                                                                                                                                                                                           Novel human protein; NHP; CUB domain; extracellular domain; obesity; high blood pressure; connective tissue disorder; i
                                                                                                                                                                                                                                                                                                                                                                  AAU00628 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a polypeptide sequence which isolated from lymph node stromal cells of fsn -/- mice. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
            (LEXI-)
                                          19-OCT-1999;
18-FEB-2000;
                                                                                       08-OCT-2000; 2000WO-US28798
                                                                                                                     26-APR-2001
                                                                                                                                                   WO200129219-A1
                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LITCLERGSHYFEEKYSKFCPAGCRDIA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASDYLLFSSATDQYGPYCGSWAVPKELRLNSNEYTVLFKSGSHISGRGFLLTYASSDHPD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.6%;
ilarity 100.0%;
Conservative
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                                                          99US-0160285
              GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                  Protein;
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Pred. No.
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                                                                        N-PSDB;
                                                                                                                                                     Donoho
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18-FEB-2000;
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CUB proteins have been associated with
cellular processes and preventing
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Novel nucleic acid encoding human for drug screening, diagnosis and

CUB-domain treatment o

of physiological disorders

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29-30;

33pp; English.

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RESULT 4
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The sequence represents a novel human protein (NHP) containing a CUB domain (an extracellular domain). CUB proteins have been associated with regulating development, modulating cellular processes and preventing
                                                             Claim
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                                                      Novel isolated human Neuropilin-Hyl and Neuropilin-Hy2 polypeptides useful for treating neurodegenerative diseases e.g. Alzheimer's disease, and for diagnosing and mapping genetic neuronal defects -
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                                                                                                                                                                                                           WPI; 2002-393966/42.
N-PSDB; AAD35992.
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06-SEP-2001; 2001US-317902P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SGSHISGRGFLLTYASSDHPDLITCLER 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 SGSHISGRGFLLTYASSDHPDLITCLER 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                 YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or trigger NHP-mediated pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                  INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
4.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Claim 3; Page 123-125; 152pp; English

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RESULT 6
AAU79459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regeneration, in wound healing, tissue repair and replacement and in healing of bones, incisions and ulcers. Compositions comprising the sequences of the invention are useful for treating diseases of periphera nervous system e.g. Parkinson's disease, Huntington's disease, Shy-Drage syndrome, amyotrophic lateral sclerosis, and traumatic disorders e.g. spinal cord disorders, head trauma and cerebrovascular diseases e.g. spinal cord disorders, head trauma and cerebrovascular diseases e.g. stroke, ulcers, immune deficiencies and immune disorders, infections by hepatitis viruses, human immunodeficiency virus (HIV), herpes viruses, mycobacteria, leishmania spp., malaria spp., autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, autoimmune thyroiditis, diabetes melliting craff-vorsus-hot disease mycothemia or artificiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       included in modulating growth regenerative capacity. treating named in modulating growth regenerative capacity. treating named in modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                organ growth; nervous system lesion; cancer; cell proliferation; cell differentiation; stem cell growth factor activity; cell discress; Huntington's disease; amyotrophic lateral sclerosis; haematopoiesis; myeloid cell disorder; lymphoid cell disorders; anaemia; platelet disorder; thrombocytopaenia; liver fibrosis; lung fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antagonists of neuropilin-like polypeptides are useful for treating cancers and other malignant diseases. Neuropilin is used to treat platelet disorders e.g. thrombocytopaenia, plastic anaemia and parox nocturnal haemoglobinuria and is used in nerve tissue growth or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; neuropilin-Hyl; chromosome 6q21; neuronal growth;
nerve regeneration; neurodegenerative disease; learning disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Neuropilin-Hyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU79459 standard; Protein; 398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth regenerative capacity, treating neurodegenerative diseases, diagnosing and mapping genetic neuronal defects and degenerative diseases like Alzheimer's disease and for treating learning and memory disease. They are also useful for inducing angiogenesis, neovascularisation, as
                                                               11-SEP-2000;
06-SEP-2001;
                                                                                                                                                             11-SEP-2001; 2001WO-US28590.
                                                                                                                                                                                                                             21-MAR-2002
                                                                                                                                                                                                                                                                                             WO200222780-A2
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              memory disorder; Alzheimer's disease; angiogenesis; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU79459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mellitus, graft-versus-host disease, myasthenia gravis and autoimmune inflammatory eye disease. The nucleic acids of the invention are used
(TANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                            reperiusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              well as organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 SGSHISGRGFLLTYASSDHP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy techniques. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSHISGRGFLLTYASSDHP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
TANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropilin-Hyl gene is located on chromosome 6q21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
н
                                                                                                                                                                                                                                                                                                                                                                                                                            food
                                                               2000US-0659671.
2001US-0659671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth and development e.g. heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to neuropilin-like polypeptide (neuropilin-Hyl
                                                                                                                                                                                                                                                                                                                                                                                                                         supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is human neuropilin-Hyl
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; 1
2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and other tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Shy-Drager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            paroxysmal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in
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DT CONTROL OF CONTROL

acquired

respiratory

Human diagnostic 04-DEC-2001 AAU19467;

(first entry)

Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemi

and therapeutic polypeptide (DITHP)

immune deficiency syndrome; AIDS;

autoimmune disorder;

Homo sapiens

RESULT 7 AAU19467

AAU19467 standard; Protein;

101 AA

밁

100

SGSHISGRGFLLTYASSDHP 119 SGSHISGRGFLLTYASSDHP 119

S

100

Query Match
Best Local Similarity
Matches 20; Conserv

Conservative

0

100.0%;

Score 20; Pred. No. Mismatches

2. .6e-1 23;

Length 398;

0; Gaps

0;

Sequence

398 AA;

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in modulating neuronal growth, regenerative capacity, treating neurodegenerative diseases, learning and memory disorders, diagnosing amapping genetic neuronal defects and degenerative diseases like Alzheimer's disease, for inducing angiogenesis, and neovascularisation and organ growth and development (e.g. the heart). The nervous systems disorders include lesions of central or peripheral nervous systems, including traumatic lesions, ischaemic lesions, infectious lesions, degenerative lesions, lesions associated with nutritional diseases or approximation of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers. The neuropilin-like proteins are useful for regulating cell proliferation, cell differentiation, sell growth factor activity for inducing proliferation of neural cells, regeneration of nerve and brain tissue, for treatment of central and peripheral nervous system diseases, and neuropathies, such as Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated neuropilin-like polypeptide including neuropilin-Hyl and neuropilin-Hy2, the full length cDNAs encoding the proteins and the coding regions of the cDNAs. Also included is a nucleic acid array comprising the cDNAs attached to a surface used for detecting full-matches or mismatches to the cDNAs. The genes for neuropilin-Hyl and Hy2 are located on human chromosome 6q21.
                                                                                                                      gene chips and as a DNA antigen.
                                                                                                                                                                                                                                                                                                                        Huntington's disease, amyotrophic lateral sclerosis, to regulate haematopolesis and treat myeloid and lymphoid cell disorders, various anaemias, and platelet disorders, such as thrombocytopaenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New neuropilin-like polypeptides for diagnosing, preventing and treating neurological conditions and disorders, cancers, and for inducing angiogenesis and neovascularisation
                                                                                   neuropilin-Hyl.
                                                                                                                                                              regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and as a food supplement or molecular weight marker. The cDNAS are useful in gene identification, genome mapping, transgenics, as hybridisation probes, for primer design,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, neurological lesions, and lesions caused by toxic substances. The neuropilin-like proteins and cDNAs are also useful as markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The nucleic acid array is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the cDNAs. The neuropilin-like proteins and encoding cDNAs are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-351881/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis and neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for detecting full-matches
                                                                                                                           The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or mismatches
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The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and treatment involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, conclude the continuous deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPs, by inserting the nucleic acids in to a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in the content of the cell cannot be used as DNA probes and therefore which patients may be in need of restorative
                                                                                                                                                                                                                                                                                                                                                                        Cheu...,
Cheu...,
Dufour GE, Flores ..
Liu TF, Roseberry AM, Ro
Wright RJ, Yap PE, Yu J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-2000;
15-MAY-2000;
16-MAY-2000;
16-MAY-2000;
16-MAY-2000;
16-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
                                                                                                                                                                                                                                                                                                   Polynucleotides encoding diagnostic enzymes, hormones and receptors, use
                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2000;
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24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-)
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24-FEB-2000;
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24-FEB-2000;
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DB; AAS31038.
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D'Sa
F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCYTE GENOMICS INC
                                                                                                                                                                                                                                                           Page 430;
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Sa SA, Ams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0184841
2000US-0185213
2000US-0185216
2000US-0203785
2000US-0204525
2000US-0204821
2000US-0204821
2000US-0204812
2000US-0205232
2000US-0204815
2000US-0205232
2000US-0205286
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Bradley DL, Brac.
SE, Jackson S
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Dahl CR, Dam TC, I
WT, Greenawalt LB, I
en BH, Russo FD, Sto
                                                                                                                                                                                                                                                                                                   stic and useful
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B, Hillman JL, Jones AL;
Stockdreher TK, Daffo A;
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Daniels
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Chang SC;

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Momiyama Gerstin E Marwaha F

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Chen

Bradley Peralta C

In SE, Altus CM, Dufour GE, Chalup MS, Hilli Wright RJ, Gietzen D, Liu TF, Yap PE, Dah dley DL, Rohatgi SD, Harris B, Roseberry AM; lta CH, David MH, Panzer SR, Flores V, Daffd AJ, Chang SC, Au AP, Inman RR;

Hillman

JL;

Dahl

Jackson

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Lincoln

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHI expression and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAU19415-AAU19625 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout; neuroprotective; antirheumatic; antiarthritic.
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                                                                                          proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; altergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic: anti-Arthronomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide comprising. Oligonucleotides and antibodies are useful for detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a biological sample, for detecting (I) in a sample, and for purifying (I) from a sample. A composition comprising (I), an agonist or antagonist is useful for treating a disease or condition associated with decreased or increased expression of functional MDDT. (I) or (II) are useful for diagnosing, treating or preventing disorders associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, and cancer and an autoimmune/inflammatory disorder such as Albarox as a steriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis rheumatoid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                                                                   ABP51461 standard; Protein;
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                                                                                                                                                                                                                                            MDDT
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for detecting differences in the chromosomal location due to
location or inversion among normal, carrier or affected individuals
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N-PSDB; WPI; 2002-527544/56 Marwaha R, Gerstin EH, Jones AL, Yı Momiyama MG, Ϋ́u Chen AJ, u JY, Wright RJ, Gietzen D, Bradley DL, Rohatgi SD, H Peralta CH, David MH, Panz Chen AJ, Chang SC, Au AP, Panzer SR, Harris Inman RR; GE, TF, Yap PE, B, Roseberry Chalup MS, Flores V, Daffo A; Hillman Dahl CR;

Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.

Claim 14; Page 603; 618pp; English.

Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for a compound for effectiveness in altering expression of a target polynucleotide comprising. Oligonucleotides and antibodies are useful for detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a biological sample, for detecting (I) in a sample, and for purifying (I) from a sample. A composition comprising (I), an agonist or antagonist is useful for treating a disease or condition associated with decreased or increased expression of functional MDDT.

(I) or (II) are useful for diagnosing, treating or preventing disorders are associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosts, hepatitis, psoriasis, and cancer and an autoimmune/inflammatory disorders such as AIDS, Addison's disease. allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatoid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology. that for cell

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                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
          and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haer
                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                          Wang
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19-JUL-2000;
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25-APR-2000;
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                                                                                                                                                                                 Example
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| 59 PDLITCLE 66
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Wang Z,
Zhou P,
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2000US-0552317.
2000US-0558042.
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2000US-0662191.
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2000US-0727344.
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Wehrman T, 2
, Goodrich R,
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Yang
                                                                                                                                                                                                                  for treating disorders
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Zhang J;
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RESULT 11
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        CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide comprises a 1 least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5pecification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence specification.
                                                                                                                                                                                                         comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide recomplementary.
                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the full-length cDNAs defined in the specification, and for the det and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                              Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                The present full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishii
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                             full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 PDLITCLE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 PDLITCLE 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T,
                                                                                                                                                                                                                                                                                                              SEQ ID-11667; 2537pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama T, Wakamats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 AA;
                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.7%;
                                                                                                                                                                                                                                                                describes primer sets for synthesising ined in the specification. Where a prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO:11667.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                              CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K, !
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito K, Y, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto
                                                                                                                                                                                                                                                                                                                                                          detection by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Matches
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06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                           06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
                                                                                                                                                                                                                                                                       06-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; proliferative disorder; inflammatory disorder; antiarrentoscaperosis; rheumatoid arthritis; transgenic; gene therapy; antiarrentosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2002
                                                                                                                                                                                                                                                                                             06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                               (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                             06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective;
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                                             2002-527544/56
DB; ABQ72618.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDDT
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8; Conserv
                                                                                                                         s
                                                                                                  WG,
                                                                                      Yu JY, Wright RJ, Gietzen D, I
IG, Bradley DL, Rohatgi SD, Harr
I, Peralta CH, David MH, Panzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
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                                                                              Chen
                                                                                                                         Lincoln
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2000US-230518P.
2000US-230519P.
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                                                                                                                                                                     2000US-231163P.
2000US-231167P.
                                                                                                                                                                                                                            2000US-230865P.
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2000US-230610P.
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2000US-230597P.
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                                                                                                               Wright RJ,
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                                                                              Chang
                                                                                                                        Altus CM,
                                                             us CM,
, Gletzen D, Liu
, Gletzen D, Liu
, Robatgi SD, Harris B, Roseu
, Rohatgi SD, Harris B, Roseu
, Rohatgi SP, Inman RR;
                                                                              SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarthritic.
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. 7.1;
                                                                                   u TF, rap.
LS B, Roseberry F
Flores V, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                         Chalup MS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                          Hillman
                                                                                                   Dahl CR;
                                                                                         Daffo A;
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            e.g.
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RESULT 13
AAM79595
ACC XXX XXX ACC XXX AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC treatment (MDDT) polypeptide (I) selected from a polypeptide having a compounce selected from 254 sequence ABP51231-ABP51484) given in the sectification, a naturally occurring polypeptide comprising a sequence (C immunogenic fragment of (I): (I) is useful for screening a compound for (C immunogenic fragment of (I): (I) is useful for screening a compound for (C immunogenic fragment of (I): (I) is useful for screening a compound for (I) preparing a polyclonal or monoclonal antibody by hybridoma technology. (C uncleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for (I) screening a compound for effectiveness in altering expression of a target polynucleotide comprising. Oligonucleotides and antibodies are useful for (I) adjunction of the compound, (I) are useful for (I) and for purifying (I) from a sample, for detecting MDDT in a sample or for assessing toxicity of a test compound, (I) are useful for (I) and for purifying (I) from a sample, for detecting (I) in a sample, (I) are useful for (I) ar
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; humanomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; vaccine; peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM79595 standard; Protein;
                                                                                                                                       05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein SEQ
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                           2001WO-US04098
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100.0%; Pr
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Pred. No. 7.1
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
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03-FEB-2000; 27-APR-2000; 20-JUN-2000;

2000US-0496914. 2000US-0560875. 2000US-0598075.

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RESULT 14
AAM40732
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Best Local S
Matches 8
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01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis: inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny, inhibin activity and may be useful in the diagnosis and/or treatment of colors of the polypeptides have the polypeptides activity.
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Zhao
21-JAN-2000;
25-APR-2000;
                                26-DEC-2000; 2000WO-US34263
                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                   22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 293;
                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                         AAM40732;
                                                                                                                                                                                                                                                                             AAM40732 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     were missing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation.
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                                                                                                                                                                                                                                                                                                                                                  119 PDLITCLE 126
                                                                                                                                                                                                                                                                                                                                         101
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)B; AAK52728.
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                                                                                                                                                                                                                                                                                                                                       PDLITCLE 108
                                                                                                                                                                                                        polypeptide
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D, Wang J,
, Wejhrman
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s system; neuropathy;
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F, Zhang J, Re
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                       The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                               Tang
Wang
Zhao
                                                                                          Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                             system, such as peripheral nervous injuries, peripheral neuropathy localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                    Sequence
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2000US-0620312.
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Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skincell proliferative disorder; cancer; tumour; autoimmune disorder; brain inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast; endocrine disorder; metabolic disorder; neurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney; chymus adrenal gland; bone marrow; prostate; s; skin; brain;

Homo sapiens.

WO200220754-A2

29-AUG-2001;

2001WO-US27127

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                                                                                                                                        The invention relates to human diagnostic and therapeutic (dithp)

polynucleotides and their associated polypeptides (DITHP polypeptides).

The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers

(e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), cendocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal disorders (e.g. ulcerative colitis, lysinuria) and transport disorders (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences ABG59943-ABG60220 represent human DITHP polypeptides of the invention.
                                                      Query Match
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Matches 8; Conserv
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07-SEP-2000;
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Jones AL,
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Marwaha
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N-PSDB; ABK71635.
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05-SEP-2000;
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101 PDLITCLE 108
                           119 PDLITCLE 126
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L, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE,
La MG, Bradley DL, Rohatgi SD, Harris B, Roseberr
EH, Peralta CH, David MH, Panzer SR, Flores V,
R, Chen AJ, Chang SC, Au AP, Inman RR;
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                                                                                                                  273 AA;
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s; Pred. No. 15;
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Irris B, Roseberry AM;
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Search completed: May 15, 2003, 13:22:40 Job time: 23.3469 secs

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OM protein -
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13:21:41 ; Search time 19.2527 Seconds (without alignments) 1093.529 Million cell updates/sec
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Perfect score: US-10-003-132-4\_COPY\_26\_244 219\_\_\_

Sequence: EELGDGCGHIVTSQDSGTMT.....NGVLSRHGSLSEKRFLFTTP 219

Scoring table: Gapop 60.0 , Gapext 60.0 OLIGO

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters:

223049

Minimum Maximum DB seq length: 100 700

Post-processing: Listing first 45 summaries

PIR\_73:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| 22 7 3.2 494 2 851117<br>23 7 3.2 507 2 T00682<br>24 7 3.2 573 2 T51239<br>25 7 3.2 578 2 B71431<br>26 7 3.2 578 2 B71431<br>27 7 3.2 51379 | 7 3.2 494 2<br>7 3.2 507 2<br>7 3.2 573 2<br>7 3.2 578 2<br>7 3.2 578 2 | 7 3.2 494 2<br>7 3.2 507 2<br>7 3.2 573 2<br>7 3.2 578 2 | 7 3.2 494 2<br>7 3.2 507 2<br>7 3.2 573 2 | 7 3.2 494 2<br>7 3.2 507 2<br>7 3.2 573 2 | 7 3.2 494 2<br>7 3.2 507 2 | 7 3.2 494 2        | 7 3 7 494 7 |     | 7 3.2 419 2        | 7 3.2 385 2        | 7 3.2 384 1        | 7 3.2 320          | 7 3.2 314 2        | 7 3.2 302 2        | 7 3.2 291          | 7 3.2 204 2        | 7 3.2 203 | 7 3.2 182 2 | 7 3.2 159 2   | 7 3.2 135 2        | 8 3.7 595 2        | 8 3.7 519 | 3.7 440 | 8 . 3.7 440 2 | 3.7 440 | 8 3.7 196 | 3.7 195 | 3.7 163 | 3.7 154            | No. Score Match Length DB ID | Result Query |
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| PWYCE              | A82847 | B85625 | G90761 | E85638 | AE0918            | S30707 | AC2259             | AC2172             | A84989             | T35913             | T40753   | S17709 | A72739 | S59306            |  |
| hypothetical prote |        | _      | _      |        | probable membrane |        | hypothetical prote | hypothetical prote | 50S ribosomal prot | hypothetical prote | hypothet |        |        | probable membrane |  |

## ALIGNMENTS

Rybelletroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant, O.; Martial, J.A. Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991

A.Title: The evolutionarily conserved Krueppel-associated box domain defines a A; Reference number: A39384; MUID:91219421; PMID:2023909

A.Accession: D39384 A;Cross-references: GB:M61869; NID:g184449; PID:g184450 C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology C;Keywords: DNA binding; zinc finger finger protein HTF6 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 08-Dec-2000 A; Molecule type: DNA A; Residues: 1-154 <BEL> A;Status: preliminary Length 154;

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Query Match Best Local 9 Matches 119 PDLITCLE 126 Local Similarity 100.0%; nes 8; Conservative ( Conservative 3.7%; Score 8; I L00.0%; Pred. No. .. Mismatches DB 2; 5. 1.7; 0; Indels 0: Gaps

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tinger protein HPF9 - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 08-Dec-2000 C; Accession: B39384

R;Bellefroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant, O.; Martial, J.A. Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991
A;Title: The evolutionarily conserved Krueppel-associated box domain defines a A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Accession: B39384

subfam

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-163 <AAA>

C; Superfamily: zinc finger protein zinc; Keywords: DNA binding; zinc finger A;Cross-references: GB:M61867 C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match Matches Local Similarity mes 8; Conserv Conservative 3.7%; Score 8; DB; 100.0%; Pred. No. 1.0 tive 0; Mismatches . 8 2 0, Length 163; Indels

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k; Hellefroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991 A; Title: The evolutionarily conserved Krueppel-associated A; Reference number: A39384; MUID:91219421; PMID:2023909 A; Accession: A39384
                                                                                                                      A;Title: The complete genome sequence of Escherichia coll A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: D65168
                                                                                                                                                                                           regulatory protein uhpC - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 30-Jun-1991 #sequence_revision 14-Nov-1997 #text_change 01-Mar-2002
C;Accession: D65168; G41853; C26925; S30078
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I.A.; Rose, D.J.; Mau, B.; Shao, Y.
 A;Cross-references: GB:AE000444; GB:U00096;
A;Experimental source: strain K-12, substrai
R;Island, M.D.; Wei, B.Y.; Kadner, R.J.
J. Bacteriol. 174, 2754-2762, 1992
                                                                    A; Molecule type: DNA
A; Residues: 1-440 <BI
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                                                                                                     A; Status: preliminary; nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:M61869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary
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                                                                    -440 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                              57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 30-Jan-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 20-Mar-1992 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human (fragment)
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                                                                                                         acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID: 9454818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8; DB 2; Pred. No. 2.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
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                                     substrain
                                                                                                       sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lecocq, P.J.; Revelant, O.; Martial, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lecocq,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . No.
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                                   NID:g2367258;
in MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAA52689.1;
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                                                                                                         shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                       translation
                                                                                                                                                             K-12
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                                                 PIDN: AAC76690.1; PID: g2367260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g184336
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                                                                                                                                                                                                               V.; Riley,
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                                                                               regulator of uhpT [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 1C;Accession: F86050
                                                                                                                                                         RESULT
F86050
                                 R; Perna, N.T.; Plunkett III, G.; iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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A; Title: Gen
A; Reference
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Genome sequence of nce number: A85480;

enterohemorrhagic MUID:21074935; PMJ

ric Escherichia PMID:11206551

Burland,

Lim,

V.; Mau, b., A.; Dimalanta,

Glasner, Lanta, E.;

J.D.; Rose, Potamousis, 14-Sep-200:

D.J.; X.; A

.; May Apoda

substrain

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regulator of uhpT [imported] - Escheric C; Species: Escherichia coli C; Date: 18-Jul-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: this is a revision to the sequence from reference A30: R;Friedrich, M.J.; Kadner, R.J. J. Bacteriol. 169, 3556-3563, 1987
J. Bacteriol. 169, 3556-3563, 1987
A;Title: Nucleotide sequence of the uhp region of Escherichia A;Reference number: A30395; MUID:87279903; PMID:3301805
A;Accession: C26925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Structure a
A; Reference number:
A; Accession: G41853
                                                                                                                                             C; Superfamily:
                                                                                                                                                                                                                                                                                                                  A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                      gasawara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                    A; Gene:
                                                                                                                                                                                                   A;Cross-references: GB:BA000007; PIDN:BAB38027.1; PID:g13364079; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                      A; Residues: 1-440 <HAY>
                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                               A; Reference number: A99629; A; Accession: D91204
                                                                                                                                                                                                                                                                                                                                                                                        R;Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: D91204
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C; Superfamily: )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 'M',87,' VCRALGAE',96,'L',98,'P',100,'L',102,'FTG',139-141,'SVNGLVFTYRA',1
A;Note: this sequence has been revised in reference A41853
C;Comment: This is one of the proteins involved in the expression of uhpT, a gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule
                                                                                       Query Match
Best Local :
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Best Local
                                                                         Matches
                                                                                                                                                                                      Genetics:
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                                  198 LANGVISR
58 LANGVLSR
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                                                                                                                                                                    ECs4604
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nce number: A41853; MUID:92234930;
                                                                                                                                                                                                                                                                                                                                                       N.; Yasunaga,
8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LANGVLSR
                                                                                                                                                                                                                                                                                                                                                                                          ₩.;
                                                                                                                                                                                                                                                            type: DNA
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                                                                     Similarity
8; Conserv
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                      Makino, K.; Ohnishi, M.;
Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hexose phosphate transport protein mbrane protein; sugar phosphate transport
                                                                                                                                               hexose phosphate transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 min
                                                                     ilarity 100.0%;
Conservative
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65
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                                                                                         Score 8;
Pred. No.
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                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Kurokawa, F
Shiba, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes for the sugar phosphate transport PMID:1569007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PIDN:AAA24726.1; PID:g148119 from reference A30395
                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transport
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                                                                                                          Length 440;
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                                                                     Indels
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PDLITCLE 126 PDLITCLE

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R;Poncelet, D.A.
submitted to the EMBL Data
                                                                           A; Cross-references: GDB:132279
A; Map position: 19p12-19p12
                                                                                                                                                   A;Status: preliminary; translated from GB/EMBI/DDBJ
A;Molecule type: mRNA
A;Residues: 1-595 <PON>
                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F; 258-291/Domain:
F; 361-394/Domain:
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A;Title: A transducin-like gene maps to the autosomal dominant polycystic kidney disease A;Reference number: A49367; MUID:94140377; PMID:8307582
                                                                                                           A;Gene: GDB:ZNF85
                                                                                                                                                                                             A; Accession: G02075
                                                                                                                                                                                                                                                                                             transcription repressor zinc finger protein 85 - human
                                                                                                                                                                                                                                                                                                                                                                       밁
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F;77-110/Domain: WD repeat homology <WD1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transducin homolog sazD - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000
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A; Residues: 1-519 <WEI>
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A; Status: pre
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                                                            Superfamily: zinc finger protein ZFP-36; LIM
                      Query Match
Best Local
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Best Local
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                     Local
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      Similarity 100
8; Conservative
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8; Conserv
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                                                                                                                                    EMBL: U35376;
3.7%; bu
100.0%; Pr
.-- 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                       Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.78;
                Score 8; u
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                                                                                                                                  NID:g1017721; PIDN:AAA79179.1; PID:g1017722
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Pred. No.
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      Mismatches
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                                                         metal-binding repeat
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                               Length 595;
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hypothetical protein Y49G5A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te
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                                                     T34009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rhodobacter capsulatus
C;Date: 07-Jun-1990 #sequence_revision
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                                                                     RESULT
                                                                                                                                                                                                                                                                                                               A; Molecule type: I
A; Residues: 1-159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Parkhill, J.; Wren, B.W.; Mungall, C.W.; Quail, M.; Rajandream, M.A.; Runature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ATP /GTP-binding protein Cj0668 [imported] -C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #te
C;Accession: D81337
                                                                                                                                                                                                                                                                 A;Gene:
                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X17433;
                                                                                                                                                                                                                                                                                                                                                                                              A; Title: DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                            R;Moreno-Vivian, C.; Schmehl, M.; Masepohl, Mol. Gen. Genet. 216, 353-363, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitrogenase (EC 1.18.6.1) molybdenum-iron protein nifx -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene:
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A; Residues: 1-135 < PAR>
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Best Local
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7; Conserv
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7; Conserv
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                                                                                                                                                                                                                                                                                            NID: 946085; PIDN: CAA35474.1;
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utherford, K.M.; VanVliet, A.; Whitehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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18;
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l, S.; Bar
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R;Becker, M.; Tin-Wollam, A.M.; Yoakum, M. submilted to the EMBL Data Library, February 1999 A;Description: The sequence of C. elegans cosmid Y49G5A. A;Reference number: 221457

C; Accession: T34009

#text\_change

29-Oct-1999

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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
                                                                                  A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-204 <KUR>
                                                                                                                                               A;Title: Genome Sequence of A;Reference number: A97359; A;Accession: C97502
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C97502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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  A; Map position:
                       A; Gene: AGR_C_2161
                                                               A;Cross-references: GB:AE007869; PIDN:AAK86972.1; PID:g15156208; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                       riboflavin synthase alpha chain (AJ236918) [imported] - Agrobacterium tumefaciens C_iSpecies: Agrobacterium tumefaciens
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A;Experimental source: strain Bristol N2; clone Y49G5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-182 <BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ster, E. W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Accession: AG2720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           riboflavin synthase alpha chain [imported] - Agrobacterium tumefaciens
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Best Local S
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                                             Genetics:
                                                                                                                                                                                                                                                                              Accession: C97502
                                                                                                                                                                                                                                                                                               Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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les 7; Conser
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les 7; Conserv
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44/3; 82/1; 102/3
circular chromosome
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                                                                                                                                                                     the Plant Pathogen and Biotechnology Agent Agrobacterium tum
PMID:11743194
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Markelz, B.
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R;Ishii, Y.; Ohno, A.; Taguchi, H.; Matsuzawa, H.; Yamaguchi, K. Antimicrob. Agents Chemother. 39, 2269-2275, 1995
A;Title: Cloning and sequence analysis of the gene for a cefotaxime-hydrolyzing class A;Reference number: I41146; MUID:96109425; PMID:8619581
A;Accession: I41146
Search completed: May 15, 2003, 13:25:58 Job time: 22.2527 secs
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A; Residues: 1-291 <ISH>
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A;Description: Cloning and the sequence analysis of a cefotaxime-hydroly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-lactamase (EC 3.5.2.6), cefotaxime-hydrolyzing - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 22-Apr-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000 C;Accession: JP0074; I41146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:D37830; NID:g1435024; PIDN:BAA07082.1; C;Superfamily: beta-lactamase I
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A; Residues: 1-89, 'D'
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A; Accession: JP0074
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Matches 7; Conserv
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ilarity 100.0%;
Conservative
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## ALIGNMENTS

RESULT 1 ZN90\_HUMAN

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| EMBL; M61870; AAA36028.1; PIR; E39384; E39384. Genew; HCMC:13165; ZNF90. MIM; 603973; InterPro; IPR000190; KRAB. InterPro; IPR00082; Znf_C2H2. Pfam; PF00096; zf-C2H2; 1. Pfam; PF00096; Zf-C2H2; 1. SMART; SM00349; KRAB; 1. SMART; SM0035; KRAB; 1. SMART; SM0035; KRAB; 1. SMART; SM0035; ZINC_FINGER_C2H2_1; 1. PROSITE; PS00028; ZINC_FINGER_C2H2_2; 1. PROSITE; PS00028; ZINC_FINGER_C2H2_2; 1. PROSITE; PS00028; ZINC_FINGER_C2H2_2; 1. PROSITE; PS00028; ZINC_FINGER_C2H2_2; 1. DOMAIN VICLEAR PROTECHIN; Repeat. DOMAIN VICLEAR PROTECHIN; Repeat. CHAB. ZN_FING 145 167 C2H2-TYPE. SMOUNTER 195 195 C2H2-TYPE. DEGENERATE). SEQUENCE 195 AA; 22562 MW; 0E808A1A62342608 CRC64; | -I- FUNCTION: MAX BE INVOLVED IN TRANSCRIPTIONAL REGULATIONI- SUBCELLULAR LOCATION: Nuclear (Probable)I- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING EMBRYONIC DEVELOPMENTI- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC- FINGER PROTEINSI- SIMILARITY: CONTAINS 1 KRAB DOMAIN.  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). | ZN90_HUMAN STANDARD; PRT; 195 AA.  Q03938; Q13938; Q1-JUN-1994 (Rel. 29, Created) Q1-JUN-1994 (Rel. 29, Last sequence update) Q1-JUN-1994 (Rel. 29, Last sequence update) Q1-CT-2001 (Rel. 40, Last annotation update) Zinc finger protein 90 (Zinc finger protein HTF9) (Fragment). ZNF90. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=91219421; PubMed=2023909; Bellefroid E.J., Poncelet D.A., Lecocq P.J., Revelant O., Martial J.A.; "The evolutionarily conserved Kruppel-associated box domain defines a subfamily of eukaryotic multifingered proteins."; Proc. Natl Acad Sci II S.A. 88.3508.3502.1901) |

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RESULT
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PRODOM; PRO0003; ZNF_C2H2; 2.
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SMART; SM00349; ZNF_C2H2; 3.
SMART; SM00355; ZNF_C2H2; 3.
SMART; SM00355; KRAB; 1.
SMART; SM00355; ZNC_FINGER_C2H2_1; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 4.
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                                                                                                                                                                                                                                                                                                             Han Z.-G., Zhang Q.-H., Ye M., Kan L.-X., Gu B.-W., E Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., "Molecular cloning of six novel Kruppel-like zinc fir hematopoietic cells and identification of a novel tradomain KRNB.";
J. Biol. Chem. 274:35741-35748(1999).
-I- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
-I- SUBCELLULAR LOCATION: Nuclear (Probable).
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He K.-L., Gu B.-W., Han Z.-G., Shen
Wang Y.-X., Chen S.-J., Chen Z.,
"Identification of genes expressed
stem/progenitor cells by expressed
length cDNA cloning.";
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O75437;
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                                                                                                                                                                                                                                    the European Bioinformatics Institute. The Tile of the European Bioinformatics Institutions as long use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=20054457;
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Mammalia; Eutheria; Primates;
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derived zinc finger protein 1
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or send a
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DNA 8:377-387(1989).
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                                                                                                                          EMBL; M27879; -; NOT_ANNO
EMBL; M61867; AAA58666.1;
PIR; B39384; B39384.
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
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ZNF117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              subfamily of eukaryotic Proc. Natl. Acad. Sci. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-166 FROM N.A. MEDLINE-91219421; PubMed=2023909; Bellefroid E.J., Poncelet D.A., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 4-418 TISSUE-Placenta;
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Mammalia; Eutheria;
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Homo sapiens (Human).
Motazoa; Chordata;
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The evolutionarily conserved Kruppel-associated subfamily of eukaryotic multifingered proteins."; Proc. Natl. Acad. Sci. U.S.A. 88:3608-3612(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bellefroid E.J.,
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                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Probable), DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY (
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8; Conserv
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InterPro; IPR001909; KRAB.
InterPro; IPR001902; Znf\_C2E
Pfam; PF00096; zf-C2H2; 10.
Pronom: PD000003; Znf\_C2H2;

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01-AUG-1992 (Rel. 2
16-OCT-2001 (Rel. 4
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MEDLINE-87279903; FubMcd=3301805;
Friedrich M.J., Kadner R.J.;

*Nucleotide sequence of the uhp region
J. Bacteriol. 169:3556-3563(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                    SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-9315143; PubMed-7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
Burland V.D., Plunkett G. 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-92234930;
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
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                                                                                                                                                                  "Island M.D., Wei B.-Y., Kadner R.J.;
"Structure and function of the uhp genes
transport system in Escherichia coli and
J. Bacteriol. 174:2754-2762(1992).
                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                 Kadner
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C2H2-TYPE.
C2H2-TYPE.
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Pred. No.
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C2H2-TYPE
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subdivision; Enterobacteriaceae;
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-TYPE (DEGENERATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                 for the sugar phosphate Salmonella typhimurium.";
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InterPro; IPR003662; sub.
InterPro; IPR003662; sub.
Pfam; PF00083; sugar_tr;
TIGREAMS; TIGR00881; 2A011
PROSITE; PS00942; GLPT; 1
                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins.";
J. Bacteriol. 175:5028-5034(1993)
-!- FUNCTION: UHPC IS REQUIRED FO
SEQUENCE FROM N.A.
MEDLINE=94140377; PubMed=8307582;
Weinstat-Saslow D.L., Germino G.G
"A transducin-like gene maps to t
kidney disease gene region.";
Genomics 18:709-711(1993).
                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                  WD-repeat protein
TBL3 OR SAZD.
                                                                                                                                                                       Q12788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M17102; AAA24722.1;
EMBL; M89479; AAA24726.1;
EMBL; L10328; AAA62019.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000444; AAC76690.1; PIR; G41853; RGECUC. EcoGene; EG11053; uhpC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                    TRANSMEM
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    -I- SUBCELLULAR LOCATION: Integral membrane protein. Inner me
    -I- SIMILARITY: BELONGS TO THE SLC37A FAMILY OF TRANSPORTERS.

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                                                                         NCBI_TaxID=9606;
                                                                                                                                        15-JUL-1998
16-OCT-2001
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8; Conser
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     transport;
                                                                                                                            36, Created)
36, Last sequence update)
40, Last annotation update)
SAZD (Transducin beta-like
                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                  R.J.;
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Pred. No.
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D8097864B7877700 CRC64;
                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                      .G.,
                                                                                                                                                                                                                                                                               Mismatches
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                      Somlo S., autosomal
                                                                                                                                                                                 519
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ng as its content is in
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                      Reeders :
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try is copyright. It is produced through Institute of Bioinformatics and the EN

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EMBL

a collaboration -

SWISS-PROT entry

SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Y2Q1;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
15-JUN-2002 (Rel. 4
               between
the Euro
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Z257_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                               This
                                                                                                                                                                                                 Han Z.-G., Zhang Q.-H., Ye M., Kan L.-X., Gu B.-W., He K.-L., Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., Chen Z., "Molecular cloning of six novel Kruppel-like zinc finger genes from the state of the sta
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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REPEAT
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PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
   use
                                                                                                                                                                                 hematopoietic cells
domain KRNB.";
                                                                                                                                                                                                                                                                                   TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                 Zinc finger protein
ZNF257 OR BMZF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00678; WD_REPEATS_1; PROSITE; PS50082; WD_REPEATS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                    J. B101.
                                                                                                                                                                                                                                                                  MEDLINE-20054457; PubMed-10585455;
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
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                                                                                                   SIMILARITY: BELG
FINGER PROTEINS
                                                                                                                                Biol. Chem. 274:35741-35748(1999).
FUNCTION: MAY FUNCTION AS A TRANSCRIPTION
SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _HUMAN
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                             SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation -
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8; Conser
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                                                                                                                  BELONGS
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257 (Bone mannotation)
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Primates;
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Catarrhini;
                                                                                                                    KRUEPPEL
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                                                                                                                  C2H2-TYPE
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                  restrictions
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Best Local
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PROSITE;
PROSITE;
                                                                                                                                                                                                 15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
EN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear
DOMAIN
                "Prediction of the coding sequences of unident The complete sequences of 100 new cDNA clones for large proteins in vitro."; DNA Res. 7:143-150(2000).
-!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION :
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY
                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf_C2H2; 9
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001909; KRI
InterPro; IPR000822; Zn1
Pfam; PF00096; Zf-C2H2;
Pfam; PF01352; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 606957;
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                                                                                      MEDLINE-20277482; PubMed-10819331;
Nagase T., Kikuno R., Ishikawa K.-I.,
                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                         Hypothetical
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PS00028; ZINC_FINGER_C2H2_1;
PS50157; ZINC_FINGER_C2H2_2;
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(Rel. 41,
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C2H2-TYPE.
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C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
22DC5B0C4613BC51 CRC64;
                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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01-OCT-1996
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.210c finger
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                Poncelet D.A., Bellefroid E.J., Bastia
Marine J.C., Pendeville H., Alami Y.,
Muller M., Martial J.A.;
                                TISSUE-Placenta;
MEDLINE-99053537; PubMed-9839802;
MEDLINE-99053537; PubMed-9839802;
                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pfam; PF01352; KRAB; 1.
PRINTS; PRODOAC
                                                                                   NCBI_TaxID=9606;
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00048; ZINCFINGER.
Probom; PD000003; Znf_C2H2; 2
SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 13.
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        "Functional analysis of ZNF85 KRAB zinc finger
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HSSP; P07248; 1/
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European Bioinformatics Institute.
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C2H2-TYPE:
482E5F1176ECA5B0 CRC64;
                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Lecocq P.J., C
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DOMAIN
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PROSITE; PS50805; KRAB; 1.

PROSITE; PS50028; ZINC_FINGER_C2H2_1; 14.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 15.

Transcription regulation; Zinc-finger; DN
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-i- FUNCTION: TRANSCRIPTIONAL REPRESSOR.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN TESTICULAR
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EMBL; M61866; AAA52689.1;
EMBL; M61868; AAA58671.1;
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TRANSFAC; T04990;
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Best Local
                                                                                            P35589;
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
15-JUL-1998 (Rel. 2
                                        Aplysia californica (Eukaryota; Metazoa; Maplysiidae; Aplysia. NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moreno-Vivian C., Schmehl M., Masepohl B., Arnold W., Klipp W.; "DNA sequence and genetic analysis of the Rhodobacter capsulatus nifENX gene region: homology between NifX and NifB suggests involvement of NifX in processing of the iron-molybdenum cofactor."; Mol. Gen. Genet. 216:353-363(1989).

-I- FUNCTION: MAY PLAY A ROLE IN THE PROCESSING OF THE IRON-
TISSUE=Ganglion;
MEDLINE=94255392;
                                                                                                                                                                                                                                                                                                 PIR; JE0031; JE0031.
InterPro; IPR003731; DUF153.
Pfam; PF02579; DUF153; 1.
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                                                                                       Synaptobrevin.
                                                                                                                                        SYB_APLCA
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8; Conser
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an email to license@isb-sib.ch).
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                                                                         (California sea hare).
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a; alpha subdivision; Rhodobacter group;
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annotation
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SEQUENCE
        This SWISS-PROT entry is copyright. between the Swiss Institute of Bioi
                                                                                                      MEDLINE=96431831; PubMed=8834913;
Bauernfeind A., Stemplinger I., Jungwirth R., Casellas J.M.;
"Sequences of beta-lactamase genes encoding CTX-M-1 (MEN-1);
2 and relationship of their amino acid sequences with those beta-lactamases.";
                                                                                                                                                                                                                                                                                Beta-lactamase
                                                                                                                                                                                                                                                                                            30-MAY-2000
30-MAY-2000
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30-MAY-2000
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                                                                                                                                                                                                                                                       Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
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                                                                                             Antimicrob. Agents Chemother.
                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                        NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001229; Synaptobrevin; 1.
PROSITE; PS00417; SYNAPTOBREVIN; 1.
Synapse; Transmembrane; Synaptosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                                                                                                                                           11 VTSQDSG 17
                                                                  imicrob. Agents Chemother. 40:509-513(1996). FUNCTION: HAS CEFOTAXIME-HYDROLYZING ACTIVITY CATALYTIC ACTIVITY: A beta-lactam + H(2)0 = a
                                            amino acid.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SYNAPTOBREVIN FAMILY.
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Kandel E., Niemann H.;
                                                                                                                                                                                                                                Proteobacteria;
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180 AA;
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(Rel. 39, Last sequence up
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ase CTX-M-2 precursor (EC 3
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RINSIC MEMBRANE PROTEIN OF SMALL
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                                    TO THE CLASS-A BETA-LACTAMASE FAMILY.
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CYTOPLASMIC (PROBABLE).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
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VESICULAR (PROBABLE);
ADC7780DA74CF347 C
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                                                                                                                                                                                                                                subdivision;
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          It is produced through a collaboration -
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PROSITE; PS00146; BETA LACTAMASE A; 1.

Hydrolase; Antibiotic resistance; Plasmid; Signal.

SIGNAL 1 28 BY SIMILARITY.

CHAIN 29 291 BETA-LACTAMASE CTX-M-3.

ACT_SITE 73 73 BY SIMILARITY.

BINDING 237 239 SUBSTRATE (BY SIMILARITY).

SEQUENCE 291 AA; 31254 MW; 2E22E251008DF7C6 CRC64;
                                                                                                                                                  InterPro; IPR000871; Beta_lacta
Pfam; PF00144; beta-lactamase;
PRINTS; PR00118; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Hydrolase; Antibiotic resistance; Plasmid;
SIGNAL 1 28 BY SIMILARITY.
                                                                                                                                                                                                                                       HSSP;
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InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam, PF00144; beta_lactamase; 1.
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Q47066; 1BZA.
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                             BLC6_SALTY 065976;
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"Two novel plasmid-mediated cefotaxime-hydrolyzing beta-
(CTX-M-5 and CTX-M-6) from Salmonella typhimurium.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: HAS CEFOTAXIME-HYDROLYZING ACTIVITY.
                                                  SALTY
                                                                                                                                                                      SEQUENCE
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InterPro; IPR000871; Beta_lactama:
Pfam; PF00144; beta-lactamase; 1.
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PROSITE; PS00146; BETA_LACTAMASE_A;
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                                                                                                                                                                     resistance; Plasmid; Signal.

BY SIMILARITY.

BETA-LACTAMASE CTX-M-5.

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SUBSTRATE (BY SIMILARITY).

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MEDLINE-SOLUTION., Taguchi H., Imajo S., Isniguro M., Meduring Ishii Y., Ohno A., Taguchi H., Imajo S., Isniguro M., Medicing Ishii Y., Ohno Agence of the gene encoding a cefotaxime-hydrolyzing "Class A beta-lactamase isolated from Escherichia coli."; class A beta-lactamase isolated from Escherichia coli."; class A beta-lactamase isolated from Escherichia coli.";
                                                                                              STRAIN=TUH12191;
MEDLINE-96109425; PubMed-8619581;
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(CTX-W-5 and CTX-M-6) from Salmonella typhimurium.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
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                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
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ISSP; Q47066; IBZA.

InterPro; IPR001466; Beta_lactamase.

InterPro; IPR000871; Beta_lactamase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
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otic resistance; plasmid; Signal.

28 BY SIMILARITY.

291 BETA-LACTAMASE CTX-M-6.

73 BY SIMILARITY.

73 SUBSTRATE (BY SIMILARITY).

239 SUBSTRATE (BY SIMILARITY).

239 CD55E4FE77531053 CRC64;
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100.0%; Pr
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precursor (EC 3.5.2.6).
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                                                                                                                                                                                                                               gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma subdivision;
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tions as long as its content
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STRAIN-TUH12191;
MEDLINE-99126537; PubMed-9925786;
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                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of the E166A mutant of extended-spectrum beta-lactamase Toho-1 at 1.8 A resolution.";
J. Mol. Biol. 285:2079-2087(1999).
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                          InterPro; IPR001466; Beta_lactamase. InterPro; IPR000871; Beta_lactamase_A. Pfam; PF00144; beta-lactamase; 1.
                                                                                                                                                                                                                                                                       EMBL;
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PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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completed: May 15, me : 9.53218 secs
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291 AA;
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A beta-lactam + H(2)0 =
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| 45                  | 44                 | 43      | 42                 | 41      | 40      | 39     | 38       | 37     | 36     | 35     | 34     | 33                 | 32                 | 31      | 30                 | 29      | 28                 | 27       | 26     | 25     | 24                 | 23                 | 22                 | 21                 | 20       | 19              | 18     | 17                 |
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| 385                 | 381                | 368     | 359                | 359     | 350     | 350    | 350      | 350    | 332    | 320    | 314    | 300                | 294                | 291     | 291                | 291     | 291                | 291      | 291    | 291    | 291                | 276                | 272                | 251                | 206      | 205             | 204    | 194                |
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| Q8X058              | Q9FNP5             | Q9GY66  | 088829             | Q9QWF8  | Q9D771  | Q9CZV9 | Q9H813 . | Q9NV85 | Q91333 | Q9XWB9 | Q97Z87 | Q8SU29             | Q93L16             | 034177  | Q8VKT5             | Q8VN22  | Q8VN23             | Q8VN24   | Q8VN25 | Q9RLX4 | Q936V5             | Q8VQ11             | Q8Y2M5             | Q31296             | Q92QU4 · | Q983B1          | Q8UG72 | Q91YF2             |
| . Q8x058 neurospora | Q9fnp5 arabidopsis | eish    | O88829 mus musculu | mus     | mus     |        |          | 5      | w      | റ      | v      | Q8su29 encephalito | Q93li6 burkholderi |         | Q8vkt5 kluyvera as |         | Q8vn23 kluyvera as | kluyvera | _      |        | Q936v5 proteus mir | Q8vq11 acinetobact | Q8y2m5 ralstonia s | Q31296 sciurus abe |          |                 | agro   | Q91yf2 mus musculu |

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# ALIGNMENTS

| PRELIMINARY; PRT; 503 AA.  (TIEMBLITEL. 17, Created) 1 (TIEMBLITEL. 17, Last sequence updi 2 (TIEMBLITEL. 17, Last sequence updi 2 (TIEMBLITEL. 17, Last sequence updi 2 (TIEMBLITEL. 17, Last annotation upl Rik protein.  RIK.  US (Mouse)  Metazoa; Chordata; Craniata; Vertel Eutheria; Rodentia; Sciurognathi; M =10090;  ROM N.A.  BL/GJ; TISSUE-TESTIS; BOOMAIN M. AS CANNIAL M. AS | CC -1- SIMIL DR EMBL; AKO |              |         |     |                                   |        |                                            |                                            |                                            |                                           |                                            | -                                          | RA Schriml I                               | RA Kuehl P.,                              | •                                          |                                            |                                  |                                  |           |                            |                         |           |  |           |          |               |        |                      |                      |                 | ID 09D4J3 | 09D4J3 |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                           | otation of a | aki Y.; | × × | Tovo-oka K., Wang K.H., Weitz C., | Sato K | P., Ring B., Ringwald M., Rodriguez I., Sa | , Marchionni L., Mashima J., Mazzarelli J. | ch S., Hill D., Hofmann M., Hume D.A., Kam | in M.J., Bult C., Fletcher C., Fujita M., | , Boffelli D., Bojunga N., Carninci P., de | , Okido T., Furuno M., Aono H., Baldarelli | L.M., Staubli F., Suzuki R., Tomita M., Wa | , Lewis S., Matsuo Y., Nikaido I., Pesole | ann W., Gaasterland T., Gissi C., King B., | ., Matsuda H.A., Ashburner M., Batalov S., | Izawa M., Nishi K., Kiyosawa H., | Hara A., Fukunishi Y., Konno H., | , Yoshino | 21085660; PubMed=11217851; | 57BL/6J; TISSUE=TESTIS; | FROM N.A. |  | Rodentia; | hordata; | ulus (Mouse). | 11RIK. | (TrEMBLrel. 21, Last | (TrEMBLrel. 17, Last | (TrEMBLrel. 17, | PRT:      |        |

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyaswa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
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                          MGD; MGI:1913936; 4631413K11Rik.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000443; LCCL_dom.
Pfam; PF00431; CUB; 1.
                                                                                                                                                                     "Functional annotation of a full-length mouse Nature 409:685-690(2001).
-i- SIMILARITY: CONTAINS 1 CUB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9D696
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01-JUN-2001
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                                                                                                                                        AK014521;
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                                                                                                                                     CONTAINS 1 CUB
BAB29409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-SKIN;
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Last sequence up
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Pred. No. 1.2e-224;
Mismatches 0;
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                                                                                                                                                                                                                          collection.";
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RESULT Q8TJT3
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AC Q8
AC Q8
DT 01
DT 01
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Q8R327
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SEQUENCE
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Q8R327;
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Q8TJT3
Q8TJT3;
Q1-JUN-2002
Q1-JUN-2002
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Similar to RIKEN cDNA 4631413K11 gene.
Mus musculus (Mouse).
                                         Hypothetical
MA3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
Submit BC026771; AAH26771.1; ...
EMBL; BC026771; AAH26771.1; ...
Archaea; Euryarchaeota; Methanococci; Methanosarcinaceae; Methanosarcinac
                             Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                  135 KYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDHPDLITCLERGSHYFEE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGLLANGVLSRHGSLSEKRFLFTTP
                                                                                                                                                                                                                                                                    KYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHY
                                                                                                                                                                                                                                                                                                                           GPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDHPDLITCLERGSHYFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGVLSRHGSLSEKRFLFTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDHPDLITCLERGSHYFEEKYSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANGVLSRHGSLSEKRFLFTTP
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145; .Consérv
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460 AA; 50334 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               432 AA;
                                                         (TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
L protein MA3694.
                                                                                                    (TrEMBLrel.
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                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               46798 MW;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 145; DB; Pred. No. 8.5
                                                                                                     Created)
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Pred. No. 1.8e-20;
                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                       219
                                                                                                                                                                                                           173
                                                                                                                                                                                                                                                                                                                                                                                                                                               AD3FB42B24CD4917 CRC64;
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             Methanosarcinales;
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Best Local s
Matches
     Q9MAA9;
Q9MAA9;
01-OCT-2000
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Galagan J.E., N.
FitzHuck
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01-DEC-2001
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Bu Allen N., Naylor J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Calvo J., Stange Thomann N., DeArellano K., John R., Stange Thomann N., Stange Th
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50805; KRAB; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2;
DNA-binding; Zinc-finger.
SEQUENCE 216 AA; 25227 MW; B5C6CF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2001) to the EMEMBL, BC008936; AAH08936.1; -.
InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF01352; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similar to DNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and physiological diversity." Genome Res. 12:532-542(2002). EMBL; AE011078; AAM07049.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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8; Conser
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     (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 21,
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(Trembirel 19, Last seq
(Trembirel 20, Last ann
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195 AA; 22019 MW;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                      126
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Primates;
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100.08; Pr
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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909E97DB7359DC67
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        sequence up
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A Deng J.M., Goldsmith A.D., Lee J.M., Ondera C.S., Quach H.L.,
A Deng J.M., Goldsmith A.D., Lee J.M., Ondera C.S., Quach H.L.,
A Carninci P., Chen H., Cheuk R., Hayashtzaki Y., Yu G., Bowser L.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Meyers M.C., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
A Davis R.W., Ecker J.R., Theologis A.;
Barabidopsis Open Reading Frame (ORF) Clones.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY091328; AAM14267.1;
BR EMBL; AY091328; AAM14267.1;
BR EMBL; AY091328; AAM14267.1;
BR EMBL; AY091328; AAM14267.1;
BR EMBL; AY091328; AAM14267.1;
SEQUENCE FROM N.A.
TISSUE-PLACENTA;
Isogai T., Ota T., Ha
Nishikawa T., Nagai K
                                                                                                                                                Q9H8G1 PRELIMINARY; PRT; 364 AA.
Q9H8G1;
01-MAR-2001 (TIEMBLrel. 16, Created)
01-MAR-2001 (TIEMBLrel. 16, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
CDNA FLJ13659 f1s, clone PLACE1011576, moderately
kruppel Irelated Zinc finger protein (HTF10) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000051;
Hypothetical protein.
SEQUENCE 336 AA; 3
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SEQUENCE FROM N.A.

Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Golds Yamada K., Onodera C.S., Quach H.L., Tang C., Toriumi M., W Lee J.M., Onodera C.S., Bowser L., Carninci P., Chen H. Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H. Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neu Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Nguyen M., Palm C.J., Sakurai T., Satou M., S Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J. Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin X., Kaul S., Town C.D., Benito M., Creasy T.H. Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC T12H1 ger Submitted (JAN-2001) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis:thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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T12H1.6 OR AT3G05100.
                                                                                                                                           Homo sapiens (Human)
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                                                                                      NCBI_TaxID=9606;
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 Hayashi K., S
i K., Sato H.,
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Primates;
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to the EMBL/GenBank/DDBJ databases.
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 Sugiyama
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InterPro; IPR000822; Znf_C2H2.
Pfam; PP01352; KRAB; 1.
Pfam; PF00096; Zf-C2H2; 3.
Pfam; PF00096; Zf-C2H2; 3.
ProDom; PD000003; Znf_C2H2; 2.
SMART; SM00349; KRAB; 1.
SMART; SM00349; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS00157; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 364 AA; 42472 MW; 5043DA4C575842B0 CRC
TIGREAMS;
PROSITE; F
        Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

EMBL; AE005598; AAG58866.1; -.

EMBL; AP002566; BAB38027.1; -.

EMBL; AP002566; BAB38027.1; -.

InterPro; IPR000849; GlpT_transporter.

InterPro; IPR000849; GlpT_transporter.

Pfam; PF00083; sugar_tr; 1.

PIGRPAMS; TIGR00881; 2A0104; 1.
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MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka Iida T., Takami H., Honda T., Sasakawa C., Ogasawara Iida T., Takami H., Honda T., Sasakawa C., Ogasawara
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                                                                                                                                                                                                                                            Apodaca J., Anantharaman T.S., Lin J., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Rose D.J., Mayhew G.F., Evans
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Escherichia coli O157:H7.
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Kimura K., Mu
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Iwayanagi T.;
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Ishida S., Murakawa K., Ono )
Murakami K., Ishii S., Kawai
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Tobe T.,
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Pfam; PF001352; KRAB; 1.

Pfam; PF00096; zf-C2H2; 10.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00349; KRAB; 1.

SMART; SM00355; ZnF_C2H2; 9.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.

PROSITE; PS01028; ZINC_FINGER_C2H2_2; 11.

DNA-Pbinding; Metal-binding; Nuclear protein; Z1

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Q9BZE6;
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SEQUENCE
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Abrink M.
           Homo
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Mammalia;
                    finger protein
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"Isolation of CDNA clones for 42 different
proteins expressed in the human monoblast c
DNA Cell Biol. 14:125-136(1995).
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Catarrhini;
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 Euteleostomi;
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Q96JC4
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Interpro; IPROUVE..,
Pfam; pF001352; KRAB; 1.
Pfam; pF00096; zf-C2H2; 12.
R Pfam; pF00096; zf-C2H2; 12.
R PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_11.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 12.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 12.
DR PROSITE; PS0157; AA; 60598 MW; F1AD4929DC67D105 CR/
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Matches 8
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InterPro; IPR001822; Znf_C2H2.

Pfam: DF00062; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and preliminary functional analysis human KRAB zinc finger proteins, HKr18 and HKr19."; DNA Cell Biol. 20:275-286(2001).
EMBL; AF277624; AAK61307.1; -.
InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KR19.
HOmo sapiens (Human).
Tharyota; Metazoa; Chordata; Metazoa; Primates;
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Pfam; PF00096; zf-C2H2; 12.
PROSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_8.
PROSITE; PS00128; ZINC_FINGER_C2H2_2; 12.
DNA-binding; Zinc_finger
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MEDLINE-21303228; PubMed-11410164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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      PDLITCLE 126
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2 (TrEMBLrel. 20,
                                                                                       Conservative
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                                                                                    Score 8; DB 4; Pred. No. 12; 0; Mismatches
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Strausberg R.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ datab.
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REMBL; BC015765; AAH15765.1;
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Pfam; PF001952; KRAB; 1.
PROSITE; PS50805; KRAB; 1.
REMOSITE; PS50805; KRAB; 1.
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EMBL; AC116548; AAL99317.1; -
SEQUENCE 132 AA; 14408 MW; 9AD15CE58D7666F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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Primates;
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Best Local
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                                                                                                       Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DaArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
                                              Pritchett M., Sowers K.R., Swanson R.V., 2 Metcalf W.W., Birren B.;
"The genome of Methanosarcina acetivorans and physiological diversity.";
Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, MA3428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reveals hypervariable sequences.",
Nature 403:665-668(2000).
EMBL; AL139076; CAB72945.1; -.
InterPro; IPR003442; UPF0079,
Pfam; PF02367; UPF0079; 1.
TIGRPAMS; TIGR00150; UPF0079; 1.
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
   Hypothetical SEQUENCE 1:
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
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01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
putative ATP /GTP-binding pr
                                                                                                                                                                                                                                                                           STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed-11932238;
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Methanosarcinaceae; Methanosarcina.
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                                 EMBL; AE011048; AAM06795.1;
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100.0%; Pred. No. 40
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proteome.
184878A5AF292852 CRC64;
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Search completed: May 15, Job time: 21.9089 secs 2003, 13:24:11

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Result
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493.221 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Packfiles1.pep:*
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US-09-186-2768-56

US-09-186-1883-56

US-09-186-18891-75

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US-08-81-853-13

US-08-850-917-13

US-08-887-3528-11

US-09-109-207C-11

US-09-109-207C-12

US-09-109-207C-12

US-09-296-005-12

US-09-296-005-12

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US-08-559-303B-77
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                                                                                                                                    Sequence 77, Application Patent No. 5824501
GENERAL INFORMATION:
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| ALIGNMENTS | US-07-668-517-17  | US-07-668-517-14  | US-07-668-517-13  | US-07-668-517-12  | US-07-668-517-11  | US-07-668-517-10 | US-07-668-517-9   | US-07-668-517-8   | US-07-668-517-6   | US-07-668-517-5   | US-07-668-517-4   | US-07-668-517-16  | US-07-668-517-3   | us-07-668-517-15  | US-07-668-517-2   | US-09-105-343A-9 | US-07-668-517-1   | US-07-994-469A-9  |
|            | Sequence 17, Appl | Sequence 14, Appl | Sequence 13, Appl | Sequence 12, Appl | Sequence 11, Appl |                  | Sequence 9, Appli | Sequence 8, Appli | Sequence 6, Appli | Sequence 5, Appli | Sequence 4, Appli | Sequence 16, Appl | Sequence 3, Appli | Sequence 15, Appl | Sequence 2, Appli | •                | Sequence 1, Appli | Sequence 9, Appli |

#### CURRENT APPLICATION NUMBER: US/09/463,702A CURRENT EILING DATE: 2000-01-24 PRIOR APPLICATION NUMBER: PCT/JP98/03114 PRIOR FILING DATE: 1998-07-10 PRIOR APPLICATION NUMBER: JAPAN 9/200387 PRIOR FILING DATE: 1997-07-25 NUMBER OF SEQ ID NOS: 44 SOFTWARE: Patentin version 3.0 SEQ ID NO 38 LENGTH: 334 TYPE: PRT ORGANISM: Escherichia coli US-09-463-702A-38 Sequence 38, Application US/09463702A APPLICANT: NATHAN A. APPLICANT: GRODEN TITLE OF INVENTION: TITLE OF INVENTION: CORRESPONDENCE ADDRESS: ADDRESSEE: AMSTER, F 7, Application US/08559303B 5824501 AGENE Research Institute, HIRAKI AND ASSOCIATES SHIMAMOTO, AKIRO FURUICHI, YASUHIRO VENTION: HUMAN GENE RECQ4 ENCODING KITAO, SAORI 90 PARK AVENUE NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA 3.2%; ilarity 100.0%; Conservative ( HIRA1150 METHODS FOR DIAGNOSIS OF BLOOM'S SYNDROME 78 ROTHSTEIN & EBENSTEIN ; Score 7; DB 4 8; Pred. No. 47; 0; Mismatches . ც DB 4; AND HELICASE 0; Length 334; TREATMENT Indels 0;

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COMPUTER READABLE FORM:

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-09-175-828-77, Application US/09175828
Sequence 77, Application US/09175828
Patent No. 6221643
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                                                                                         OPERATING SYSTEM: MS-D
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                            FILING DATE: PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE

COMPUTER: IBM PC COMPATIBLE
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REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                         UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                          DRRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 3.2%;
Local Similarity 100.0%;
mes 7; Conservative (
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OTHER INFORMATION:
                                                                                                                                                                                               COUNTRY: U
                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08, FILING DATE: NOVEMBER 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                             CITY: NEW YORK
                                                                                                                                                                                                                                                                              ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELIZABETH A. BOGOSIAN
                                                                                                                                                                                                                            NEW YORK
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(212) 28
                                                                                                                                                                                                                                                            90 PARK AVENUE
                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                          NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z
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NOVEMBER 15, 1995
INFORMATION:
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286-0854 or 286-0082
                                                                                                                              MS-DOS
                                                                                                                                                                                                                                                                                                                          METHODS FOR DIAGNOSIS OF BLOOM'S SYNDROME
                                                                                                                                                                                                                                                                             ROTHSTEIN & EBENSTEIN
                           us/08/559,303
                                                                             US/09/175,828
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RESULT 5
US-09-186-276B-56
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US-09-334-601-4
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                                                                                                                       Sequence 56,
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09334601 Patent No. 6280989
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CURRENT FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 77:
                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
  TITLE
               APPLICANT
                                                                                                                                                                                                                                                                                                            LENGTH: 414
TYPE: PRT
ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION:
HYPOTHETICAL:
ANTI-SENSE: NO
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241 LQSKGIS 247
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                                                                                                                                                                                         261 VIVLEKS 267
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                                                                                                                                                                                                                                           Local Similarity
ses 7; Conserv
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STRANDEDNESS: SINGLE
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                                                                             INFORMATION:
ANT: Benfey, Philip
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                                                                                                            6388173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELIZABETH A. BOGOSIAN RATION NUMBER: 39,911
                                     Wysocka-Diller,
Malamy, Jocelyn
                                                                                                                       Application US/09186276B
                                                                   DiLaurenzio,
              Helariutta, Yrjo
                          Pysh, Leonard
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Scarecrow Gene, Promoter and Uses Thereof
                                       Jocelyn E.
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100.0%; Pr
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                                                   Joanna
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Pred. No.
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CURRENT APPLICATION NUMBER:

REFERENCE: 5914-075-999

RIOR APPLICATION NUMBER: 08/842,445

1998-11-05

US/09/186,276B

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; LOCATION: (1)...(52
; OTHER INFORMATION:
US-09-186-276B-56
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SEQ ID NO 56
SEQ THE 524
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 524
TYPE: PRT
                                                                                                                                                 Sequence 56, Application US/09186188B Patent No. 6455672
                                                                                                                        APPLICANT: Benfey e
                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
           CURRENT APPLICATION NUMBER: US/09/186,188B
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR FILING DATE: 1997-04-24
                                                                         APPLICANT: Benfey et al.
TITLE OF INVENTION: Scarecrow Gene, Promoter
TITLE OF INVENTION: Thereof
FILE REFERENCE: 5914-074-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/842, CURRENT FILING DATE: 1997-04-24 EARLIER APPLICATION NUMBER: 08/638,617 EARLIER FILING DATE: 1996-04-26
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 52
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Scarecrow Gene, Promoter TITLE OF INVENTION: Thereof FILE REFERENCE: 5914-056-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Benfey et al.
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PRIOR APPLICATION NUMBER: 08/638,617
PRIOR FILING DATE: 1996-04-26
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Plant
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                                                                                                                                                                                                                                                                                                                              Local Similarity
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APPLICATION NUMBER: 08/638,617
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644127
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                                                                                                                                                                                                                                                                                                             red. No. 72
Mismatches
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o. 72;
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5. 72;
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                                                                                                                                                                                                                                                                                                                                            Length 524;
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Best Local Similarity
Watches 7; Conserve
                                                                                            TOPOLOGY: US-08-781-891-75
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-186-188B-56
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                              Query Match
Best Local S
Matches 7
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LENGTH: 524
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                                                                                                                                                                                     TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Plant
                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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186 LQSKGIS 192
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                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 27-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
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                              Similarity 7; Conserv
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                                                                                                                                      amino acid
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                                                                                                                                                     607 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                              3.2%; Score 7; DB 3; llarity 100.0%; Pred. No. 82; Conservative 0; Mismatches
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Pred. No. 72;
0; Mismatches
                                                          Length 607;
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US-08-796-414B-3
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APPLICANT: Wendy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (517) 347-4103
TELEX: NO. 5876987e
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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REFERENCE/DOCKET NUMBER: MS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,414B
FILING DATE: February 6, 1997
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                                                                                                                                                                                         ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
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NAME: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                  PUBLICATION INFORMATION:
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                                                                                                                                                                                                                           CELL TYPE:
                                                                                 IDENTIFICATION METHOD: OTHER INFORMATION:
                                  TITLE:
                                                                                                                                                                                                                                                              TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Lir
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VOLUME:
                  JOURNAL:
                                                  AUTHORS:
                                                                                                                      NAME/KEY: D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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US-08-241-853-13
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US-08-241-853-13
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
                                                                                                                                                                                                        TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                   TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                  HYPOTHETICAL:
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84 EKIITV 89
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                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                         35 EKIITV 40
                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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CITY: Hackensack
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100.0%; Pred. N
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                                                   Mismatches
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                                             DB 1; L., No. 1.6e+02; 0;
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; Sequence 13, Application US/08850917 ; Patent No. 5854045

RESULT 11 US-08-850-917-13

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GENERAL INFORMATION:

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US-08-887-352B-11
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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APPLICATION NUMBER: US 0
FILING DATE: 12-MAY-1994
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/850,917 FILING DATE: 02-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                     COUNTRY:
                                                                                                                                    STREET:
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                                                                                                                SSEE: Genentech, Inc.
F: 1 DNA Way
South San Francisco
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                                                                                                                                                                                                                                Henry B. Lowman, Leonard G. Presta,
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Hanafusa, Hidesaburo
JENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
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                                                                                                                                                                                  Improving Polypeptides 26
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Pred. No.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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APPLICANT: Henry
                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,
                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                  TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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                                                                                           TOPOLOGY:
                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/887,352B FILING DATE: 03-Jul-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
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Improved Anti-IgE Antibodies
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No. 1.7e+02;
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Antibodies and Method of
               .7e+02;
                                           Length 114;
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RGSHYF 103

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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-114
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-11
                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-12
Search completed: May 15, 2003, 13:24:51 Job time: 14.0644 secs
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US-09-109-207C-12
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SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09109207C Patent No. 6172213 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/109,207C CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR FILING DATE: 1997-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1
                                                                                                              127 RGSHYF 132
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                                                                            98 RGSHYF 103
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0; Mismatches
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                                                                                                                                                      Mismatches
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b. 1.7e+02;
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Perfect score:
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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9 US-09-759-13-77

10 US-09-753-14-8

10 US-09-712-363-14-8

10 US-10-253-007-56

10 US-10-253-007-56

10 US-09-815-242-10414

10 US-09-8164-761-47749

10 US-09-910-150-21

10 US-09-910-150-21

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Sequence 51, Appl
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181 GHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLFTTP 219

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Query Match Best Local ( Matches

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y Match 100.0%; Score 219; DB 9; 1 Local Similarity 100.0%; Pred. No. 1.3e-204; hes 219; Conservative 0; Mismatches 0;

Length 503; Indels

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| RESULT 1 US-10-003-132-4 Sequence 4, App Sequence 4, App Publication No. APPLICANT: FORMA APPLICANT: GA APPLICANT: GA APPLICANT: GA APPLICANT: APPLICANT: CURRENT APPLICA FILE REFERENCE CURRENT FILING PRIOR APPLICA CURRENT FILING D NUMBER OF SEQ NUMBER OF SEQ SOFTWARE: Fast SEQ ID NO 4 LENGTH: 503 TYPE: PRT ORGANISM: Mus US-10-003-132-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 4444499876654<br>5444499876654<br>54436654                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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| 132-4 4, Applion No. 11NFORMAI NT: FOX. NT: GACNT:  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Application No. US200201 ORMATION: Fox, Brian A Gao, Zeren Shoemaker, NVENTION: NEU ENCE: 00-62 PPLICATION NUMBE LING DATE: 200 SEQ ID NOS: 1 FastSEQ for W Mus musculus  Mus musculus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Lication US/10003132 US20020192750A1 US20020192750A1  Brian A.  Zeren  Demaker, Kimberly E. TION: NEUROPILIN HOM: 00-62 WITION NUMBER: US/10/ DATE: 2001-11-15 ION NUMBER: US 60/24 UTE: 2000-11-15 UD NOS: 19 ED for Windows Vers musculus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 118<br>121<br>121<br>123<br>123<br>123<br>123<br>123<br>123<br>123<br>123                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| \$ 131 TO 00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 1100<br>1100<br>1100<br>1100<br>1100<br>1100<br>1100<br>110                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ALIGNMENTS 0003132 A1 LIVE. LI | US-09-910-150-23 US-09-920-171-3 US-09-920-171-3 US-09-920-171-3 US-09-920-171-10 US-09-796-692-2374 US-09-925-179-3 US-09-925-179-3 US-09-925-29-800 US-09-925-29-800 US-09-925-29-800 US-09-925-29-800 US-09-925-29-800 US-09-925-29-800 US-09-925-29-801 US-09-925-29-801 US-09-925-29-801 US-09-925-29-801 US-09-925-29-801 US-09-925-29-801 US-09-931-16-378-28 US-09-766-3018-1 US-09-756-3018-1 US-09-934-465-13 US-09-934-465-13 US-09-934-465-13 US-09-936-5358-1 US-09-956-51618-1 US-09-756-1618-1                                                                                                                                                                                                                                                                                                                                                            |
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US-09-823-038A-51

Sequence 51, Application US/09823038A

Patent No. US20020058335A1

INFORMATION

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; ORGANISM: Mouse
US-09-823-038A-51
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                                                                                                                 Best Local Similarity Matches 100; Conserv
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                       SEQ ID NO 6
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SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 503
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                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/249,004 PRIOR FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gao, Zeren
APPLICANT: Shoemaker, Kimberly E.
TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCUB5
FILE REFERENCE: 00-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fox, Brian A. APPLICANT: Gao, Zeren
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/823,038A
CURRENT FILING DATE: 2001-07-09
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TITLE OF INVENTION: Compositions Isolated From Stromal Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
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TYPE: PRT
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180 GGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLFTTP 219
                                     100 DLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDEL 159
                                                                         120 DLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDEL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDLNIESKTC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASDYLLFSSATDQYGPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDHPD 145
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Onrust, Rene
                                                                                                                   Conservative
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                                                                                                                                45.7%;
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                                                                                                           Score 100; DB 9; L; Pred. No. 5.2e-89;
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RESULT 5
US-09-759-130B-75
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                                                                             GENERAL INFORMATION:
                                                                                              Sequence 75, Application US/09759130B Publication No. US20030022279A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 76
                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: Millennium Pharmaceuticals, APPLICANT: McCarthy, Sean A APPLICANT: Fraser, Christopher C APPLICANT: Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: MPIOO-5350MNIM
CUTRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/559,497 PRIOR FILING DATE: 2000-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 421
TYPE: PRT
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                                                                                                                                                                                                                                         100 SGSHISGRGFLLTYASSDHPDLITCLER 127
                                                                                                                                                                                                                  100 SGSHISGRGFLLTYASSDHPDLITCLER 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/420,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/393,996 FILING DATE: 1999-09-10 APPLICATION NUMBER: US 09/602,871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/596,194
FILING DATE: 2000-07-14
APPLICATION NUMBER: US 09/342,364
FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/333,159 FILING DATE: 1999-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-05-24
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Holtzman, Douglas A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09759130B
No. US20030022279A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barnes, Thomas S
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                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kevin R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charles R
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                                                                                                                                                                                                                                                                                                                    12.8%;
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                                                                                                                                                                                                                                                                                                                                       Length 421
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                                                     CURRENT APPLICATION NUMBER: US/10/309/389
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: 09/425.488
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: JP 9-184184
PRIOR FILING DATE: 1997-07-09
PRIOR APPLICATION NUMBER: US 09/112,563
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: JP 11-148603
PRIOR APPLICATION NUMBER: JP 11-148603
PRIOR FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                US-10-309-389-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-759-130B-75
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 75
LENGTH: 681
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Best Local 9
                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                          TITLE OF INVENTION: Sialyltransferase and DNA encoding the same FILE REFERENCE:
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CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
FITTE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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FILING DATE: 2000-01-07
APPLICATION NUMBER: US 09/559,497
FILING DATE: 2000-04-27
APPLICATION NUMBER: US 09/578,063
FILING DATE: 2000-05-24
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    359
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Similarity 100.0%;
28; Conservative 0;
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Test, Susan (Thar)
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                                                                                                                                                                                                                                                                                                   Masaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 09/393,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 681; 7e-19;
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B 8

186 LQSKGIS 192 ||||||| 241 LQSKGIS 247

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Query Match
Best Local Similarity
Thes 7; Conserve
                                                                  OTHER INFORMATION: S: US-09-753-143-77
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US-09-753-143-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                   TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 77: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIDM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION NUMBER: US/09/753,143

APPLICATION NUMBER: US/09/753,143

FILING DATE: 02-Jan-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/175,828

FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 VTVLFKS 212
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nes 7; Conserv
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                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME
                                                                                                                                                                 FEATURE:
                                                                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NATHAN A. ELLIS, JAMES GERMAN,
                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                              NAME: ELIZABETH A. BOGOSIAN REGISTRATION NUMBER: 39,911 REFERENCE/DOCKET NUMBER: 63475/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NEW YORK COUNTRY: U.S.A.
                                                                                                                   IDENTIFICATION METHOD:
                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: NEW YORK
                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                            DESCRIPTION:
                                                                                                                                                                                                                                         TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)
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                                                                                                                                                                                                                                                                                       ENGTH:
              Conservative
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100.0%;
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                                                                                       SEQ ID NO:
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Pred. No
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Pred. No.
              Mismatches
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                              No.
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                            DB 10;
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o. 1e+02;
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                                         Length 370;
            Indels
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US-09-712-363-148

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RESULT 9
US-10-253-007-56
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                                          SOFTWARE: Fas
SEQ ID NO 56
LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/10253007 Publication No. US20030088073A1 GENERAL INFORMATION:
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LENGTH: 385
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                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/253,007
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: US/09/186,188
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR FILING DATE: 1997-04-24
PRIOR FILING DATE: 1997-04-24
                                                                                                       PRIOR APPLICATION NUMBER: 08/638,617
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
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APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 5914-074-999
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Scarecrow Gene, Promoter and TITLE OF INVENTION: Thereof
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-02-01
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PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
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CURRENT FILING DATE: 2000-11-13
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PRIOR FILING DATE: 1999-05-14
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PRIOR FILING DATE: 2000-01-28
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ORGANISM: Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 LILRLGD 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/
FILING DATE: 1999-05-14
APPLICATION NUMBER: 60/
                                                                                       FastSEQ
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                                                                                       for Windows Version 3.0
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100.0%; Pred. N
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Best Local Similarity
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; NAME/KEY: VARIANT

; LOCATION: (1)...(524)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-10-253-007-56
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; TYPE: PRT
; ORGANISM: Bovine Serum Albumin
US-10-045-170A-1
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US-10-045-170A-1
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Best Local Similarity 100
Matches 7; Conservative
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                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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APPLICANT: Wang, Jack
APPLICANT: Hewick, Rodney
TITLE OF INVENTION: ACID-LABILE ISOTOPE-CODED EXTRACTANT (ALICE) AND
TITLE OF INVENTION: MASS SPECTROMETRIC ANALYSIS OF PROTEIN MIXTURES
FILE REFERENCE: GI5412AUSA
                                                                                                                                              TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA, 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/242643
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 16
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CURRENT FILING DATE: 2001-10-22
            PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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11 LLESSAT 17
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APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                                                                                                           0414, Application US/09815242
US20020061569A1
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                                                                                                                                                                                                                                       Carr, Grant
                                                                                                                                                                                                                       Yamamoto, Robert T.
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100.0%; Pred. No.
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o. 1.6e+02;
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o. 1.4e+02;
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US-09-815-242-10414
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Best Local
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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                                                                         APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/180,312
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APPLICATION NUMBER: PCT/US01/00662
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  FILING
                                      FILING DATE:
                                                       APPLICATION NUMBER: US 09/608,408
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Chen, Wensheng
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2000-06-30
NUMBER: US 09/774,203
2001-01-29
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100.0%; Pred. No. 1.
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-911-777-5
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                                                                                                                                                  US-09-864-761-47562
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US-09-911-777-5
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Best Local S
Matches
                                                                                                                Sequence 47562, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 5
                                                                                                   GENERAL INFORMATION:
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Best Local
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47749
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                    APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR FILING DATE: 1999-07-09
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CURRENT FILING DATE: 2001-07-24
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EST_HUMAN HIT: AW406955.1, EVALUE 1.00e-01
SWISSPROT HIT: P01871, EVALUE 7.00e-03
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PRIOR APPLICATION NUMBER: US 60/207,456

APPLICATION NUMBER: US 60/180,312 FILING DATE: 2000-02-04

URRENT APPLICATION NUMBER: US/09/864,761
URRENT FILING DATE: 2001-05-23

Aeomica-X-1

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                                                                                                                                      RESULT 15
US-09-910-150-21
                                                                                  Sequence 21, Application US/09910150 Patent No. US20020068698A1 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                Matches
APPLICANT: Millennium Pharmaceuticals, APPLICANT: Meyers, Rachel APPLICANT: Rudolph-Owen, Laura APPLICANT: Kapeller-Libermann, Rosana APPLICANT: Tsai, Fong Ying
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les 6; Conserv
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FILING DATE: 2001-01-30
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b; Pred. No. 3.1
0; Mismatches
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IN FETAL LIVER, SIGNAL = 1.6
HIT: AW799294.1, EVALUE 2.00e-47
HIT: P23201, EVALUE 8.80e-01
                                                                    Inc.
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; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-910-150-21
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Search completed: May 15, 2003, 13:26:36 Job time: 12.6892 secs
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                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: 13237, 18480, 2245 OR 16228 NOVEL HUMAN TITLE OF INVENTION: PROTEIN KINASE MOLECULES AND USES THEREFOR FILE REFERENCE: 38155-20020.00 CURRENT APPLICATION NUMBER: US/09/910,150 CURRENT FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                    LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                 198 LANGVL 203
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Gapop 10.0 , Gapext 0.5
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1475.448 Million cell updates/sec
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SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:

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| DR XX PR XX |                                     |                                                          |                                |              |                 |         |                                                                                                                                                                                                                                                                                        |                                                                     |                           |           |                                                       |                |                |                                        |                                        |                                       |                                       |                                                                                      |                                        |                                                            |                               |                               |                               |                                 |                                                                  |                               |                                 |                                                                   |                                                                |                          |                                                                 |                                        |                                              |                |
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| Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD; Murison JG; WPI; 2000-664924/64.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | (GENE-) GENESIS RES & DEV CORP LTD. | 25-MAR-1999; 99US-0276268.<br>26-AUG-1999; 99US-0383586. | . 18-FEB-2000; 2000WO-NZ00015. | 05-OCT-2000. | WO200058463-A1. | Mus sp. | Lymph node stromal cell; fsn -/- mice; inflammatory disorder; immune system disorder; cancer; viral disorder; HIV infection; blood vessel growth; tumour necrosis factor disorder; arthritis; inflammatory bowel disease; fibroblast growth factor-mediated disorder; cardiac failure. | Polypeptide isolated from lymph node stromal cells of fsn -/- mice. | 19-FEB-2001 (first entry) | AAB19126; | RESULT 1 AAB19126 AAB19126 standard; Protein; 503 AA. | . ALIGNMENTS . | 150.5 5.6 1192 | 150.5 5.6 1111 22 AAU00197 Human novel | 150.5 5.6 1084 22 AAU00718 Human novel | 150.5 5.6 718 22 AAU00200 Human novel | 150.5 5.6 717 22 AAU00196 Human novel | 150.5 5.6 689 22 AAU00713 Human novel  <br>  150.5 5.6 690 22 AAU00717   Human novel | 153.5 5.7 728 22 AAB85060 Human serine | 154 5.8 464 22 AAM93631 Hu<br>153.5 5.7 728 22 AAB47559 Pr | 157 5.9 315 22 AAB75323 Human | 161.5 6.0 3623 20 AAY27020 Ra | 162.5 6.1 3631 22 ABG28277 NO | 164.5 6.2 419 22 ABG22064 Novel | 168 6.3 415 22 AAB88415 Human<br>164.5 6.2 415 20 AAY31743 Human | 169 6.3 372 22 AAB80229 Human | 170.5 6.4 415 21 AAB24404 Human | 170.5 6.4 75 23 ABG45349 Human<br>170.5 6.4 415 20 AAY13361 Amino | 170.5 6.4 75 22 AAM/5913 Human 170.5 6.4 75 22 AAM/36024 Pepti | 170.5 6.4 75 22 AAM63102 | 177.5 6.6 686 23 AAE14564 Human 170.5 6.4 75 22 ABB42217 Pentid | 181.5 6.8 686 23 AAE14568 Human MASP-2 | 436.5 16.3 669 21 AAY70539 Human Factor 8 Ho | Novel<br>Human |

Result No.

Score

Query Match

Length

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Description

503 515 539 586 487 398 398 385

AAB19126 AAU00670 AAU00629 AAU00628 AAU00628 AAE22715 AAE22715 AAU79459 AAG75450

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SUMMARIES

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                                                                                                                                                                                                                                                     ARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVARKGSTFRPMDTDTEEV
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                                                                                   THKHSHSSGGFPPATGATQVESYQRPASPKPVGGGYDKPAASSFLDSRDPASQSQMTSGG
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1; Mismatches
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2.6e-243;
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RESULT 2 AAU00670 ID AAU0

AAU00670 standard; Protein;

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Query Match Best Local

Similarity

72.1%; 55.8%;

Score Pred.

No. 2.4

5; DB 22; .4e-173;

Length 715

Sequence

715

AA;

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cc survival, differentiation, activity, morphology, or movement/migration color, e.g. T cells and cells of the heart, liver, pancreas, placenta, cc brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral cc blood leukocyte, bone marrow or thymus tissue. They can be used as condulating agents for regulating cellular processes, thus, the proteins cc and their associated nucleic acids can be used to prognosticate, prevent, cc diagnose, or treat disorders associated with physiological processes. Cc These disorders include abnormal blood coagulation, asthma, anaphylaxis, cc thepatitis, multiple sclerosis, cancer, coronary artery disease, malaria, catopic dermatitis, amyotrophic lateral sclerosis, maningitis, attention cc deficit disorder, Crohn's disease, gastroenteritis, goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and cmuscular dystrophy, Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immuno-competent cycretebrate and harvesting blood or serum from the vertebrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents human TANGO 229 polypeptide. This protein and similar others exhibit the ability to affect growth, proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid molecule for diagnosis, therapy of human and other animal disorder, or as regulating cellular processes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mackay CR, Myers PS,
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/note= "Transmembrane domain"
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            08-OCT-2000; 2000WO-US28798
                                                                                                                     Novel human protein; NHP; CUB domain; extracellular domain; obesity; high blood pressure; connective tissue disorder; if
                                                                                                                                                           Novel human protein (NHP) sequence #3
                                                                                                                                                                                    29-AUG-2001
                                                                                                                                                                                                             AAU00630;
                                     26-APR-2001
                                                             WO200129219-A1
                                                                                     Homo sapiens.
                                                                                                            NHP-mediated
                                                                                                                                                                                                                                    AAU00630 standard;
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                                                                                                            pathway.
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18-FEB-2000; 2000US-0183583
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           286 DAQKTGCWKQIKYPFARHQSTEFTISYDNEKEMTQKLDLITSDMA
                                  434 TKKEDETITRPIPSEETSTGINITTVAIPLVLLVVLVFAGMGIFAAFRKKKKKGSPYGSA
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Pred. No. 3.9e-115;
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Best Local Similarity
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N-PSDB;
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                                                                                    SGSHISGRGFLLTYASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGY 184
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1 MTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMGIFAAFRKKKKKGSPYGSAEAQKTDCWKQIKYPFARHQSAEFTISYDNEKEMTQKLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCPAGCRDVAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGIL
                                                                                                                                                                                                         neuropilin-Hyl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237;
                                                                                                                                                                      neuropilin-like polypeptide; neuropilin-Hyl; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487
                                                                                                                                                                                                                                                                                                                                                                                                                   486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TTPGMNITTVAIPSVIFIALLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1154.5; T
Pred. No. 1.7e-1
4; Mismatches
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                                                                                                                                                                                                                                                            Novel isolated human Neuropilin-Hy1 and Neuropilin-Hy2 polypeptides useful for treating neurodegenerative diseases e.g. Alzheimer's disease, and for diagnosing and mapping genetic neuronal defects
                                                                                                                                                                                                                                                                                               WPI; 2002-393966/42
N-PSDB; AAD35992.
                                                                                                                                                                                                                                                                                                                                                        11-SEP-2000;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                cerebroprotective;
immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; nootropic; neuroprotective; vulnerary; anticonvulsant; antiparasitic; cerebroprotective; tranquilliser; virucide; antibacterial; cytostatic; immunosuppressive; chromosome 6q21.
                                                                                                                                                                                                                                                                                                                                                                                                                 W0200222815-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                        2000US-0659671.
2001US-317902P.
                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US28488
                                                                                                                                                                                                                                                                                                                                                                                                                                                6q21.
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Claim 3; Page 123-125; 152pp; English

The invention relates to neuropilin-like polypeptide (neuropilin-Hyl and CC neuropilin-Hyl) and their corresponding nucleic acids. The neuropilin-CC like polypeptides and polynucleotides are useful in modulating neuronal CC growth regenerative capacity, treating neurodegenerative diseases, CC diagnosing and mapping genetic neuronal defects and degenerative diseases (Clike Alzheimer's disease and for treating learning and memory disorders. CC They are also useful for inducing angiogenesis, neovascularisation, as CC well as organ growth and development e.g. heart and other tissues. CC Antagonists of neuropilin-like polypeptides are useful for treating cancers and other malignant diseases. Neuropilin is used to treat CC platelet disorders e.g. thrombocytopaenia, plastic anaemia and paroxysmal CC nocturnal haemoglobinuria and is used in nerve tissue growth or CC regeneration, in wound healing, tissue repair and replacement and in the conturnal haemoglobinuria and ulcers. Compositions comprising the CC sequences of the invention are useful for treating diseases of peripheral nervous system e.g. Parkinson's disease, Huntington's disease, Shy-Drager CC syndrome, amyotrophic lateral sclerosis, and traumatic disorders e.g. cmpositions conters, infections by hepatitis viruses, human immunodeficiency virus (HIV), herpes viruses, compositions by hepatitis viruses, human immunodeficiency virus (HIV), herpes viruses, culorimune pulmonary inflammation, autoimmune thyroiditis, diabetes inflammatory eye disease. The nucleic acids of the invention are used in classes. The nucleic acids of the invention are used in inflammatory eye disease. The nucleic acids of the invention are used gene therapy techniques. The present sequence is human neuropilin-Hyl protein. Neuropilin-Hyl gene is located on chromosome 6q21. 'n

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Sequence 398 A,

Query Match

Local

Similarity

26.8%;

Length

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                     64
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                    CLERGSHYFEEKYSK-FCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDELGGH
                                                                     GDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILKLGDLNIESKTCASD
                                                             GDGCGHLYTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASD
                                                                                                     Conservative
                                                                                                     36;
                                                                                                  Score 715; DB 23; I
Pred. No. 6.7e-59;
Pred. No. 6.7e-59;
Mismatches 60;
                                                                                                     Indels
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                                        148
  205
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RESULT 7
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 밁
                                              The invention relates to an isolated neuropilin-like polypeptide CC including neuropilin-Hy1 and neuropilin-Hy2, the full length cDNAs (CC encoding the proteins and the coding regions of the cDNAs. Also included CC is a nucleic acid array comprising the cDNAs attached to a surface used CC for detecting full-matches or mismatches to the cDNAs. The genes CC for neuropilin-Hy1 and Hy2 are located on human chromosome 6q21. CC The nucleic acid array is useful for detecting full-matches or mismatches CC to the cDNAs. The neuropilin-like proteins and encoding cDNAs are useful CC in modulating neuronal growth, regenerative capacity, treating CC neurodegenerative diseases, learning and memory disorders, diagnosing and CC mapping genetic neuronal defects and degenerative diseases like and compan growth and development (e.g. the heart). The nervous systems and clading traumatic lesions, ischaemic lesions, infectious lesions, including traumatic lesions, ischaemic lesions, infectious lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-2000;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nerve regeneration; neurodegenerative disease; learning disorder; memory disorder; Alzheimer's disease; anglogenesis; neovascularisation; organ growth; nervous system lesion; cancer; call proliferation; cell differentiation; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                        New neuropilin-like polypeptides for diagnosing, preventing treating neurological conditions and disorders, cancers, and inducing anglogenesis and neovascularisation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; haematopoiesis; myeloid cell disorder; lymphoid cell disorders; anaemia; platelet disorder; thrombocytopaenia; liver fibrosis; lung fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neuropilin-Hyl; chromosome 6q21; neuronal growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU79459
                                    degenerative lesions, lesions associated with nutritional diseases or
                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-351881/38
N-PSDB; ABK49565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TANG/) TANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reperfusion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INLLQSKGISHYEGLLANGVLSRHGSLSEKRF----LFTTPGMNITTVAIPSVIFIALLL 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                 neurological lesions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    food supplement; DNA microarray.
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2001US-0659671.
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                                                                                                                                                                                                                                                                                                                                                     144pp; English.
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and lesions caused by cDNAs are also useful
                   toxic
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ckers for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferation, cell differentiation, stem cell growth factor activity, for inducing proliferation of neural cells, regeneration of nerve and brain tissue, for treatment of central and peripheral nervous system diseases, and neuropathies, such as Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, to regulate haematopoiesis and treat myeloid and lymphoid cell disorders, various anaemias, and platelet disorders, such as thrombocytopaenia, regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and as a food supplement or molecular weight marker. The cDNAS are useful in gene identification, genome mapping, transgenics, as hybridisation probes, for primer design, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene chips and as a DNA antigen. The present sequence represents
WPI; 2001-235357/24
                          Ruben
                                                                                 29-SEP-1999;
03-NOV-1999;
                                                                                                                                                         05-APR-2001.
                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                            colorectal
                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                      Human colon
                                                                                                                                                                                                                                                                                                               03-SEP-2001
                                                                                                                                                                                                                                                                                                                                          AAG75450;
                                                                                                                                                                                                                                                                                                                                                                      AAG75450 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuropilin-Hy1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancers. The neuropilin-like proteins are useful for regulating cell
                                                                                                                           28-SEP-2000;
                                                                                                                                                                                    WO200122920-A2
                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGDRPSEKTLDQQSRTFLATGTTFVKDSFS---TDG---TSLLCKAAIHAGIIADELGGQ 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PHMIVWHSGKTREGSIAAEEEGVPKLYLVIQKQELVQDLVLVATVGCSRSLSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISVLQRKGISRYEGILANGVLSREFEIFREQLFSSVLFYSWGNTVHAV-----IELMF
                          , MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                          Barash SC,
                                                                                                                                                                                                                                            carcinoma
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                                                                                                                                                                                                                                                                                    cancer antigen
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99US-0163280.
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54.3%;
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Pred. No. 6.7e-59;
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N-PSDB; AAH34855

09-AUG-2002

(first entry)

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the proteins are collectively known as colon cancer antigens. The cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevent diagnosis and treatment of diseases associated with inappropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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OPLOPR-
                                RPASPKPVGGGYDKPAASSFLDSRDPASQSQMTSGGDDGYSAPRNGLAPLNQTAMTAL 502
                                                                                                                                                           KGSTFRPMDTDTEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPEYATPIVERHLLRAH
                                                                                                                                                                                                                                     GCWKQIKYPFARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTV----AR
                                                                                                                                                                                                                                                                                                                                                             HGYRDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLFLLLLVLLLLLEDAGAQQGDGCGHTVLGPESGTLTSINYPQTYPNSTVCEWEIRVKM
                                                                    PTQWQQKIAMKMELLGCQFIPKGRPPKLTQPPPPRNSNDLKNTTA--PPKIAKGRAPKFT
                                                                                                                                                                                                                                                                                       KTSGCYGTLGMESGVIADPQITASSVLEWTDHTGQENSWKPKKARLKKPGPPWAAFATDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSVLALLFAVCAPLRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPK 67
                                                                                                                                          KWTVYREPGVEQDKI-----FQGNKDY-HQDVRNXF-LP-----PIIAR-FIRVN
                                                                                                                                                                                                                                                                                                                       TTP-----GMNITTVAIPSVIFIALL----LTGM-GIFAICRKRKKKGNPYVSADAQKT
                                                                                                                                                                                                                                                                                                                                                                                                 DGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFKSGSHISGRGFLLTYASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTK 18:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and AAG73514 to AAG77788 cleic acid molecules (N) a
                                                                                                                                                                                                               -IDLNKEKKIT---GIITTGITMVEHNYYVSAYRILYSDDGQ
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Pred. No. 2.6e-43;
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                                                                                                      -PGPRPTHKHSHSSGGFPPATGATQVESYQ
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Human; neuropilin-like polypeptide; neuropilin-Hy2; neovascularisation; neurodegenerative disease; Alzheimer's disease; learning; angiogenesis; thrombocytopaenia; memory; platelet; plastic anaemia; antiinflammatory; ophthalmological; paroxysmal nocturnal haemoglobinuria; protozoacide; vound healing; tissue repair; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Shy-Drager syndrome; trauma; spinal cord; cerebrovascular; stroke; ulcer; immune; infection; multiple sclerosis; human immunodeficiency virus; HIV; autoimmune disorder; dermatological; systemic lupus erythematosus; rheumatoid arthritis; antithyroid; cancer; sutoimmune thyroiditis; diabetes mellitus; graft-versus-host disease; myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; nootropic; neuroprotective; vulnerary; anticonvulsant; antiparastic; cerebroprotective; tranguillser; virucide; antibacterial; cytostatic; immunosuppressive; chromosome 6g21.
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Homo sapiens.

Rey Location/Qualifiers
Peptide 1..20
Perotein 61..385
Protein 61..385

/note= "Human mature neuropilin-Hy2 protein"

WO200222815-A1.

12-SEP-2001; 2001WO-US28488

11-SEP-2000; 2000US-0659671 06-SEP-2001; 2001US-317902P

(HYSE-) HYSEQ INC

Tang YT;

WPI; 2002-393966/42 N-PSDB; AAD35994.

Novel isolated human Neuropilin-Hyl and Neuropilin-Hy2 polypeptides useful for treating neurodegenerative diseases e.g. Alzheimer's disease, and for diagnosing and mapping genetic neuronal defects

Claim 3; Page 128-130; 152pp; English

The invention relates to neuropilin-like polypeptide (neuropilin-Hyl and neuropilin-Hyl) and their corresponding nucleic acids. The neuropilin-like polypeptides and polypucleotides are useful in modulating neuronal growth regenerative capacity, treating neurodegenerative diseases. It is alzahemer's disease and for treating learning and memory diseases like Alzahemer's disease and for treating learning and memory diseases. They are also useful for inducing angiogenesis, neovascularisation, as well as organ growth and development e.g. heart and other tissues. Antagonists of neuropilin-like polypeptides are useful for treating cancers and other malignant diseases. Neuropilin is used to treat platelet disorders e.g. thrombocytopaenia, plastic anaemia and paroxysmal necturnal haemoglobinuria and is used in nerve tissue growth or regeneration, in wound healing, tissue repair and replacement and in healing of bones, incisions and ulcers. Compositions comprising the sequences of the invention are useful for treating diseases of peripheral nervous system e.g. Parkinson's disease, Huntington's disease, Shy-Drager syndrome, amyotrophic lateral sclerosis, and traumatic disorders e.g. spinal cord disorders, head trauma and cerebrovascular diseases e.g. multiple sclerosis, systemic lapus seythematosus, rheumatoid arthitis, autoimmune pulmonary inflammation, autoimmune thyroiditis, diabetes

RESULT 9
AAE22716
ID AAE2
XX
AC AAE2

AAE22716

AAE22716 standard; Protein; 385

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RESULT 10
AAU79460
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Best Local :
                                                                                                                                                                                                                                                                                                                  organ growth; nervous system lesion; cancer; cell proliferation; cell differentiation; stem cell growth factor activity; cell disease; Huntington's disease; amyotrophic lateral sclerosis; haematopoiesis; myeloid cell disorder; lymphoid cell disorder; anaemia; platelet disorder; thrombocytopaenia; liver fibrosis; lung fibrosis; platelet disorder; thrombocytopaenia; liver fibrosis; lung fibrosis;
                                                                  11-SEP-2000;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mellitus, graft-versus-host disease, myasthenia gravis and autoimmune inflammatory eye disease. The nucleic acids of the invention are used gene therapy techniques. The present sequence is human neuropilin-Hy2
                                                                                                                                     21-MAR-2002
                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                    nerve regeneration; neurodegenerative disease; learning disorder;
memory disorder; Alzheimer's disease; anglogenesis; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neuropilin-Hy2; chromosome 6q21; neuronal growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Neuropilin-Hy2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU79460 standard; Protein; 385 AA.
                                      (TANG/) TANG
                                                                                                          11-SEP-2001; 2001WO-US28590.
                                                                                                                                                                 WO200222780-A2
                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                      reperfusion;
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            TY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GERVRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropilin-Hy2 gene is located on chromosome 6q21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 AA;
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                                                                  2000US-0659671
2001US-0659671
                                                                                                                                                                                                                                                                                                      food supplement; DNA microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                         /label= Signal_peptide
21..385
/label= Mature_neuropi
                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                           Mature_neuropilin_Hy2
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Pred. No. 1
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Sequence

385

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neurodegenerative diseases, learning and memory disorders, diagnosing and mapping genetic neuronal defects and degenerative diseases like Alzhelmer's disease, for inducing angiogenesis, and neovascularisation and organ growth and development (e.g. the heart). The nervous system disorders include lesions of central or peripheral nervous systems, including traumatic lesions, inchaemic lesions, infectious lesions, degenerative lesions, lesions associated with nutritional diseases or disorders, neurological lesions, and lesions caused by toxic substances. The neuropilin-like proteins and cDNAs are also useful as markers for cancers. The neuropilin-like proteins are useful for regulating cell proliferation, cell differentiation, sem cell growth factor activity, for inducing proliferation of neural cells, regeneration of nerve and brain tissue, for treatment of central and peripheral nervous system diseases, and neuropathies, such as parkinson's disease, contains and peripheral nervous system tentior of a disease and neuropathies, such as parkinson's disease.
                                                                              Huntington's disease, amyotrophic lateral sclerosis, to regulate haematopoiesis and treat myeloid and lymphoid cell disorders, var. anaematas, and platelet disorders, such as thrombocytopaenia, regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and as a food supplement or molecular weight marker. The cDNAS are useful in gene identification, genome mapping, transgenics, as hybridisation probes, for primer design, gene chips and as a DNA antigen. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for detecting full-matches or mismacures to the cDNAs. The neuropilin-lyl and Hy2 are located on human chromosome 6q21. The nucleic acid array is useful for detecting full-matches or mismatches to the cDNAs. The neuropilin-like proteins and encoding cDNAs are useful to the cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         including neuropilin-Hy1 and neuropilin-Hy2, the full length cDNAs encoding the proteins and the coding regions of the cDNAs. Also inc is a nucleic acid array comprising the cDNAs attached to a surface for detecting full-matches or mismatches to the cDNAs. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated neuropilin-like polypeptide including neuropilin-Hy1 and neuropilin-Hy2, the full length cDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New neuropilin-like polypeptides for diagnosing, preventing and treating neurological conditions and disorders, cancers, and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-351881/38.
N-PSDB; ABK49567.
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                                                                                                                                                       GERVRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITL
                                                              DGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLF
                                                                                                    LFMSGIHVSGRGFLASYSVIDKQDLITCLDTASNFLEPEFSKYCPAGCLLPFAEISGTIP
                                                                                                                    LFKSGSHISGRGFLLTYASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTK 181
                                                                                                                                                                               GKRLILRLGDLNIE-SKTCASDYLLFSS----ATDQYGPYCG-SWAVPKELRLNSNEVTV 121
                                                                                                                                                                                                                                   PSVLALLFAVCAPLRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPK 67
                                                                                                                                                                                                         PLFLLLLLVLLLLLEDAGAQQGDGCGHTVLGPESGTLTSINYPQTYPNSTVCEWEIRVKM 61
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245
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                                                                                                                                                                                                                                                                                     Length 385;
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АВВ97386

ABB97386 standard; Protein;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and \mathtt{multiple} \cdot \mathtt{sclerosis} -
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DB; ABN32572.
                                                TTPG
                                                                                                                                                DGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLF
                                                                                                                                                                                                                                                                                                        GERVRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITL
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                                                                                               HITTHE HI
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KTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Wehrman
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Pred. No. 1
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: RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombolysis e.g. to treat
to treat inflammatory conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
.5e-41;
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AAE22721
ID AAE
cerebrovascular; stroke; ulcer; immune; infection; multiple sclerosis; human immunodeficiency virus; HIV; autoimmune disorder; dermatological; systemic lupus erythematosus; rheumatoid arthritis; antithyroid; cancer; autoimmune thyroiditis; diabetes mellitus; graft-versus-host disease; myasthenia gravis; autoimmune inflammatory eye disease; gene therapy; nootropic; neuroprotective; vulnerary; anticonvulsant; antiparasitic; cerebroprotective; tranquilliser; virucide; antibacterial; cytostatic; immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurodegenerative disease; Alzheimer's disease; learning; angiogenesis; thrombocytopaenia; memory; platelet; plastic anaemia; antiinflammatory; ophthalmological; paroxysmal notetur; plastic anaemia; portozoacide; wound healing; tissue repair; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Shy_Drager syndrome; trauma; spinal cord; amyotrophic lateral sclerosis; Shy_Drager syndrome; trauma; spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neuropilin-Hy2 mature protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuropilin-like polypeptide;
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WO200222815-A1

21-MAR-2002.

12-SEP-2001; 2001WO-US28488

11-SEP-2000; 2000US-0659671. 06-SEP-2001; 2001US-317902P.

WPI; 2002-393966/42

Novel isolated human Neuropilin-Hyl and Neuropilin-Hyl polypeptides useful for treating neurodegenerative diseases e.g. Alzheimer's disease, and for diagnosing and mapping genetic neuronal defects -

Disclosure; Page 131-132; 152pp; English.

CC diagnosing and mapping genetic neuronal defects and degenerative diseases (CC like Alzheimer's disease and for treating learning and memory disorders.)

CC well as organ growth and development e.g. heart and other tissues.

CC Antagonists of neuropilin-like polypeptides are useful for treating CC cancers and other malignant diseases. Neuropilin is used to treat (CC platelet disorders e.g. thrombovytopeenia, plastic anaemia and paroxysmal (CC regeneration, in wound healing, tissue repair and replacement and in the healing of bones, inclsions and ulcers. Compositions comprising the composition of the invention are useful for treating the sequences of the invention are useful for treating the compositions system e.g. Parkinson's disease, Huntington's diseases, Shy-Drager (CC syndrome, amyotrophic lateral sclerosis, and traumatic disorders e.g. syndrome, amyotrophic lateral sclerosis, and traumatic disorders e.g. compositions viruses, human immunodeficiency virus (HIV), herpes viruses, myothockeria, Leishmania app., malaria app., autoimmune disorders e.g. compositions of the invention, autoimmune thyroiditis, diabetes (compositions systemic plumos erythematosus, rheumatoid arthitis, autoimmune pulmonary inflammation, autoimmune thyroiditis, diabetes (conformations) and users used in the invention are used in a folial of the invention are used in the properties of the invention are used in the inventi The invention relates to neuropilin-like polypeptide (neuropilin-Hy1 and neuropilin-Hy2) and their corresponding nucleic acids. The neuropilininflammatory neuropilin-Hy2) and their corresponding nucleic acids. The new like polypeptides and polynucleotides are useful in modulating eye disease. The nucleic acids of the invention neuronal

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RESULT 13
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Matches 106;
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haematopoietic, heart and reproductive tissues. It has haemostatic and cerebroprotective activities. The F8H contains a Factor 5/8 signature and is useful as a therapeutic for treating cogulation related diseases such as haemophilia and stroke. The nucleic acid is useful as such as haemophilia and stroke. The nucleic acid is useful as hybridisation probe and amplification primer for detecting deficiencies in the level of F8H mRNA, for screening F8H gene mutations and for monitoring regulation of gene expression. Fragments of the nucleic acid are also useful as diagnostic probes and primers, and can be used in screening methods such as those using DNA chips. The present sequence is also useful as a target to screen therapeutically useful modulators
                                                                                                                                                                                                       Factor 8 treating
                                                                                                                                a coagulation cofactor which is selectively expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Factor 8 Homologue; F8H;
cerebroprotective; therapeutic;
                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                 The present sequence is a human Factor 8 homologue (F8H),
                                                                                                                                                                                 Claim
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                                                                                                                                                                              3; Page 64-66;
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Pred. No. 9
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.9e-41;
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stroke
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Homo sapiens

17-MAY-2002

AAE14565;

Human mature

MASP-2 (first entry)

protein.

Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorde

AAE14565

AAE14565 standard; peptide; 671

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 DGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GERVRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITL 61
                                                                                                                                                                                                                                                                ALAAVLVPVLVMVLTTLILILVCAWHWRNRKKKTEGTYDLPY----WDRAGWWKGMKQEL 477
                                                                                                                                                                                                                                                                                                                         NSNDLKNTTAPPKIAKGRAPKFTQPLQPRSSNEFPAQTEQTTASPDIRNTTVTPNVTKDV
                                                                                                                                                                                                                                                                                                                                                                               GNKDYHQDVRNNFLPPIIARFIRVNPTQWQQKIAMKMELLGCQFIPKGRPPKLTQPPPPR 361
                                                                                                                                                                                FRPMDTDTEEVRVNTEASGH-----YDCPHRPGRHEYALPLTHSEPEYATPIVERHLLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKRLILRLGDLNIE-SKTCASDYLLFSS----ATDQYGPYCG-SWAVPKELRLNSNEVTV 121
                                                                  SFLDSRD-----PASQSQMTSGGDDG
                                                                                                                                                                                                              PAKAVDHEETPVRYSSSE--VNHLSPREVT---TVLQADSAEYAQPLVGGIVGTLHQRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFKSGSHISGRGFLLTYASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTK 181
                                                                                                                          HTFSTQSGYRVPG-PRPTHKHSHSSGGFPPATGATQVESYQRPASPKPVGGGYDKP-AAS
                                                                                                                                                    FKP----EE----GKEAGYADLDPYNSPGQEVYHAYAEPLPITGPEYATPII-----
                                                                                                                                                                                                                                        -----ARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVARKGST
                                                                                                                                                                                                                                                                                             AIPSVI--FIALLLTGMGIFAIC-----RKRKKKGN---PYVSADAQKTGCWKQIKYPF
                                                                                                                                                                                                                                                                                                                                                                                                                                    YQWLQIDLNKEKKITGIITTGSTMVEHNYYVSAYRILYSDDGQKWTVYREPGVEQDKIFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTSGCYGTLGMESGVIADPQITASSVLEWTDHTGQENSWKPKKARLKKPGPPWAAFATDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGYRDSSPLCMAGVHAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLSTSLFTF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFMSGIHVSGRGFLASYSVIDKODLITCLDTASNFLEPEFSKYCPAGCLLPFAEISGTIP 121
                                                                                              ---MDMSGHPTTSVGQPSTSTFKATGNQPPPLVGTYNTLLSRTDSCSSAQAQYDTPKAGK
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Pred. No. 4.2e-32;
0; Mismatches 155;
                                                                     483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
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17-MAY-2002

(first entry)

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RESULT 15
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AC AAE14
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                        AAE14568 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 45; Page 73-76; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUL-2000;
01-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jensenius JC, Thiel
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(THIE/) THIEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections
                                                                                                                                                                                                    345
                                                                                                                                                                                                                                             191 CKAAIHAGIITDELGGHINLLQSKGISHYEGLL 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSGQVFTQRSGELSSPEYPRPYPKLSSCTYSISLEEGFSVILDFVESFDVETHPETLCPY 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLIL---RLGDLNIESKT-CAS
                                                                                                                                                                                               ACSIVDCGPPDDLPSGRVEYITGPGVTTYKAVI 377
                                                                                                                                                                                                                                                                                                                                             -----PDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNT-----KDGYRDTSLL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                            DYLLFSSATDQYGPYCGSWAVPKELRLNSNEVTVLF---KSGSHISGRGFLLTYASSDH- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-179791/23
                                                                                                                                                                                                                                                                                              CPYPMAPPNGHVSPVQAKYILKDSFSIFCETGYELLQGHLPLKSFTAVCQKDGSWDRPMP
                                                                                                                                                                                                                                                                                                                                                                                                 DFLKIQTDREEHGPFCGK-TLPHRIETKSNTVTITFVTDESGDH----TGWKIHYTSTAHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is human mature MASP-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                          686 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 181.5; DB 23
Pred. No. 6.9e-08;
12; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived from
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Query Match Best Local S Matches

Similarity

Conservative

42;

Mismatches

Indels Length

Gaps

7;

686; 25;

Score 181.5; Pred. No. 7.

.1e-08; DB 23; Sequence

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2222
                             levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human MASP-2 protein. Note: The present sequence is stated as being the same as SEQ ID NO:2 shown in figure 6 of the specification (AAEI4564). However the sequences differ at various locations.
                                                                                                                                                                                          mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast, retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or
                                                                                                                                          multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or
                                                                                                                                                                                                                                                                                                                                                                                          Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-2000; 2000DK-0001089.
01-JUN-2001; 2001DK-0000870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder
                                                                                                                                                                                                                                                                                                            The invention relates to use of a polypeptide derived from
                                                                                                                                                                                                                                                                                                                                            Claim 41; Page 71-73; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-179791/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jensenius JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JENS/) JENSENIUS J C. (THIE/) THIEL S.
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156
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16..686
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**metalloproteinase** 

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Post-processing: Minimum Match
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2671
1 MGTGAGGPSVLALI
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Gapop 10.0 , Gapext 0.5
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procollagen C-endo
procollagen C-endo
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CRP-ductin-alpha p
tolloid-BMP-1 like
UVS.2 protein - Af
procollagen I C-pr
dorsal-ventral pat
procollagen C-endo
procollagen C-endo
                                                                                                    membrane type-seri
                                                    coagulation factor
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                                                                                                                                                                                                                                                F;19-134/Domain: CIr/Cls repeat homology <CIRI>
F;142-180/Domain: EGF homology <EGFF>
F;184-293/Domain: CIr/Cls repeat homology <CIR2>
F;380-361/Domain: complement factor H repeat homology <FH1>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;445-679/Domain: trypsin homology <FN2>
F;445-679/Domain: trypsin homology <FN2>
F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-5
F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F;483,532,633/Active site: His, Asp, Ser #status predicted
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A;Accession: A59271
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R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Y09926; NID:94007626; PIDN:CAA71059.1; PID:94007627
A;Experimental source: tissue liver
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the amino end of the mature prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-686 <JEN>
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A;Map position: 1p36.2-1p36.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB:MASP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              superfamily: complement subcomponent Clr; Clr/Cls repeat homology; c
Keywords: beta-hydroxyasparagine; complement pathway; duplication; h
;l-15/Domain: signal sequence #status predicted <SIG>
;l6-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
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Best Local
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                                                                       DYLLFSSATDQYGPYCGSWAVPKELRLNSNEVTVLF---KSGSHISGRGFLLTYASSDH-
                                                                                                                                                    CGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLIL---RLGDLNIESKT-CAS
                                                  DFLKIQTDREEHGPFCGK-TLPHRIETKSNTVTITFVTDESGDH---TGWKIHYTSTAHA
                                                                                                                  CSGQVFTQRSGELSSPEYPRPYPKLSSCTYSISLEEGFSVILDFVESFDVETHPETLCPY 243
                                                                                                                                                                                       1 Similarity
52; Conserv
                                                                                                                                                                                       6.8%; ilarity 24.4%; Conservative
                PDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNT-----KDGYRDTSLL 190
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A47100
T23345
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T23345
T000062
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Pred. No. 7.3e-06;
2; Mismatches 94;
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Result No.

Match Query

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A; Accession: T30337
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C; Species: X
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F;444-681/Domain: trypsin homology <TRY>
F;180,412/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-21/Domain: signal sequence #status predicted <SIG>
F;17-133/Domain: Clr/Cls repeat homology <ClR>
F;22-694/Product: serine protease homolog #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement C; Keywords: differentiation; glycoprotein; hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Sakai, H.; Nakashima, S.; Yoshimura, Gene 209, 87-94, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement subcomponent C 1SBAR.GIF (EC 3.4.21.42) C;Species: Rattus norvegicus (Norway rat) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                             A; Molecule type: mRNA
                                                                             A; Status: preliminary; translated
                                                                                                                              A; Description:
                                                                                                                                           submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: DDBJ:D88250; NID:g3080541; PIDN:BAA25797.1; P.C.;Comment: This protein is involved in glial cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-694 <SAK>
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Best Local S
Matches 52
                                                                                                                                                                                       olyprotein - African clawed frog
;Species: Xenopus laevis (African clawed frog)
;Date: 22-Oct_1999 #sequence_revision 22-Oct-1999
   Query Match
                                                  Residues:
                                                                                                                                                                        Accession: T30337
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                                                                                                                                                                                                                                                                                                                                                                 DLTGQNKGWKLRY----HGDPIPCPKEISANSIWEPEKAKYVFKDVVKITCVDGFEVVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                            VLTIRREDFDVEPADSEGNCHDSLTFAAKNOOFGPYCGNGFPGPLTIKTOSNTLDIVFOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAVCAP - - - LRIQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRL
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                                  EMBL: U81290;
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                                                                                                                           of ovochymase,
                                                                                                                                         Hedrick, J.L.
ibrary, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <EGF>
                                NID:g2981640; PID:g2981641; PIDN:AAC24717.1
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Pred. No. 6.3
   Score 168;
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   1524;
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F;1-20/Domain: signa
F;21-3623/Product: 1
F;133-164/Domain: EC
F;436-467/Domain: EC
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F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of A;Reference number: Z16459; MUID:98148073; PMID:9478979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision i1-Jun-1999 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T08618
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R; Moestrup, S.K.; Kozyraki, R.; Kristiansen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-3623 <M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               932 CGEVLTA-STGIIESPGHPNVYPRGVNCTWHVVVQRGQLIRLEFSSFYLEFHYNCTNDYL 990
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GTVARKGSTFRPMDTDTEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPEYATPIVERH
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                                                                                                                                                            LAVFDGPTTNSRLIDKLCGDTTPAPIRSNKDVVLLKLRTDAGQQGRGFEINFRQRCDN--
                                                                                                                                                                                                                 --LFTTPGMN----
                                                                                                                                                                                                                                                                  TGCGGNLTTPTGVLTSPNYPMPYYHSSECYWRLEASHGSPFELEFQDFHLEHHPSCSLDY
                                                                                                                                                                                                                                                                                                                                                                        ---EIRDGGYETSPL--VGIYCGSVLPPTIISHSNKLWLKFKSDAALTAKGFSAYWDGSS 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDYTDNFGMLSSPNFPNNYPSNWECIYRITVGLNQQIALHFTDFTLEDYFGSQCVDFV-- 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LFSSATDQY-GPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSD-----
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                                                    --VVIVNKTSGILESINYP
                                                                                                        PYVSADAQKTGCWKQIKYPFARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGT
                                                                                                                                                                                                                                                                                                                         EGLLAN-----GVL-----
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                                                                                                                                                                                                              ITTVAIPSVIFIALL-----LTGMGIFAICRKRKKGN
                                                                                                                                                                                                                                                                                                                         -----SRHGSLSEKRF-----
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Pred. No. 0.00094;
4; Mismatches 189;
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3; Mismatches
                                                    -- NPYDKNQRCNWTIQATTGNTVNY-----
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A; Residues: 1-3623 < KO;
A; Cross references: EM
C; Genetics:
A; Map position: 10p12
C; Superfamily: intrins:
C; Keywords: receptor; V
    F;141-177/Domain: E
F;181-293/Domain: C
F;300-360/Domain: C
F;365-428/Domain: C
                                    A;Cross-references: EMBL:X16160; NID:g49621; PIDN:CAA34286.1; PID:g49622
A;Note: part of this sequence, including the amino ends of both the heavy and light C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement fact C;Keywords: beta-hydroxysaparagine; calcium binding; duplication; glycoprotein; hydr:F:1-21/Domain: signal sequence #status predicted <SIG>F:1-21/Domain: C1r/C1s repeat homology <C1R1>F:17-133/Domain: C1r/C1s repeat homology <Chain #status experimental <HCH>F:141-177/Domain: C1r/C1s repeat homology <C1R2>F:141-197/Domain: C1r/C1s repeat homology <C1R2>F:181-293/Domain: C1r/C1s repeat homology <C1R2>F:181-293/
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                                                                                                                                                                                                                                                                                             TEBS Lett. 250, 411-415, 1989
A;Title: Complete primary structure of a calcium-dependent A;Reference number: S05008; MUID:89325606; PMID:2753140
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S05008
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A; Residues: 1-695 < KIN>
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R; Kinoshita, H.;
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted
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A; Residues: 1-3623 < KOZ>
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A; Status: pre
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A; Title: The
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3593-3600,
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411-415, 1989
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28.5%;
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Pred. No. 0.0
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C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal C:Superfamily: Xenopus A5 antigen; CIr/Cls repeat homology; discoidin I amino-termina C:Reywords: duplication; glycoprotein; transmembrane protein F:1-21/Domain: signal sequence #status predicted <SIG>F:22-927/Froduct: A5 antigen #status predicted <A5A>F:27-138/Domain: CIr/Cls repeat homology <CIRI>F:147-262/Domain: CIr/Cls repeat homology <CIRI>F:2147-262/Domain: CIr/Cls repeat homology <CIRI>F:274-424/Domain: discoidin I amino-terminal homology <DN1>F:430-584/Domain: discoidin I amino-terminal homology <DN2>F:648-812/Domain: discoidin I amino-terminal homology <DN2>F:648-812/Domain: transmembrane #status predicted <TMA>F:150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted <TMA>F:150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Date: 10-Sep-1333 To 20948
C; Accession: JH0466; JQ0948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:D10467; A; Experimental source: tadpole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Takagi, S.; Hirata, T
Neuron' 7, 295-307, 1991
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F;446-695/Product: serine proteinase lig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA.
A; Residues: 1-927 < TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: The A5 antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JH0466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 antigen precursor - African clawed frog
Species: Xenopus laevis (African clawed frog)
Spate: 10-Sep-1999 **Sequence_revision 10-Sep-1999 *text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 FAVCAP---LRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRL
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AKEGFFANFSV-
                                               SGRGFLLTYASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGYRDTSL
                                                                                                      EADSNAPGGQTCRYDWLGIWDGFPGVGPHIGRYCGQ-NTPGRVRSFTGILSMIFHTDSAI
                                                                                                                                                     ES-----KTCASDYL----LFSSATDQYGPYCGSWAVPKELRLNSNEVTVLFKSGSHI 129
                                                                                                                                                                                                          IRYEVFKTGPECSRNFTS-SNGVIKSPKYPEKYPNALECTYIIFAPKMQEIVLEFESFEL
                                                                                                                                                                                                                                                              LRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDLNI
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66; MUID:91337458;
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                                                                                                                                                                                                                                                                                                                   Score 157; DB 1;
Pred. No. 0.00087;
0; Mismatches 177
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A;Title: Molecular characterization of a novel serine protease involved in activation A;Reference number: I54763; MUID:94289349; PMID:8018603 A;Accession: I54763
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                                                                                                                                                                                                                                                                                            F;19-135/Domain: C1r/C1s repeat homology <C1R1>
F;143-181/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-234,'E',236-284,'G',286-498,'K',500-542,'K',544-642,'S',644-699
A;Cross-references: DBBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP A;Cross-references: GDB:361104; GDB:330954; OMIM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M. Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the Cls family of complement proteins found in a A;Reference number: JN0883; MUID:94059062; PMID:8240317
A;Accession: JN0883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-699 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ra-reactive factor (EC 3.4.21.-) 1 N; Alternate names: mannose binding
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                                                                                                                                                                                                                                                                                                                                          Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; Reywords: beta-hydroxyasparagine; complement pathway; duplication; Reywords: beta-hydroxyasparagine; complement pathway; duplication; 1-17/Domain: signal sequence #status predicted <STG>;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Accession:
                                                                           :490,552,646/Active site:
                                                                                             159/Modified site: erythro-beta-hydroxyasparagine (Asn) *status 448-449/Cleavage site: Arg-Ile (autolytic) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:D28593; NID:g790963; PIDN:BAA05928.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Species: Homo sapiens (man);Date: 19-May-2000 #text_change;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change;Accession: I54763; JN0883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                          367-432/Domain: complement factor H rel
449-691/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comment: This is a serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated
                                                                                                                                                                                                                                                                      185-294/Domain:
                                                                                                                                             ,178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441
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  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T.; Endo, Y.; Matsushita, M.; Fujita, munol. 6, 665-669, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFTGNTDATDVVYRPFSKPVITRFVRLRPVTWEN--GISLRFELYGCKITDYPCSRMLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESYQRPASPKPV----GGGYDKPAASSF 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WLQIDLAEEKIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVSGLISDSQITASSQVDRNWVPELARLVTSRSG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TGTVARKGST-FRPMDTD--TEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNITTVAIPSVIFIALLLTGMGI-FAICRKRKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLFT----TPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -YATPIVERHLLRAHTFSTQSGYRVPGPRPTHKHS-----HSSGGFPPATGATQV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDTVKEWIQVDLENLRFVSGIGTQGAISKETKKKYFVKSYKVDISSNGEDWITLKDGNKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCWKQIKYPFARHQSTEFT----ISYDNEKEMTQKLDLITSDMADYQQPLMIG
                                                                                                                                                                                                                   complement factor H repeat homology complement factor H repeat homology
                                                                                                                                                                                                                                                                      Clr/Cls repeat homology <ClR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GVIIQGGK--HKENKVFMRKFKIGYSNNG-----TEW
  5.7%;
23.0%;
                                                                      His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bactericidal factor that
                                                                    Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
Score 151.5; DB 1; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor - human
protein-associated
                                                                      Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -HFDQISVSSQYSMNWSAERSRLNYVENGWTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMIM: 600521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activates
                                                                                                                                                                                                                      <FH1><FH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine proteinase 1 (MASP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---WALPPSNTHPYTKE
                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g471128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement C4
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                                                                                                                      predicted
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                                                                                                                                                                 A;Title: The serine proteinase chain of human complement A;Reference number: A05140; MUID:84104122; PMID:6362661 A;Accession: A05140
                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 356-513, 'G', 514-688 <TO2>
R; Carter, P.E.; Dunbar, B.; Fothergil
Biochem. J. 215, 565-571, 1983
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                      A; Title: Human complement component Cls. Partial sequence A; Reference number: A25396; MUID:86164350; PMID:3007145
                                                                                     A;Molecule type: protein
A;Residues: 438-483,'X',485-500;503-534;542-558;561-572,'A',574-601;617-623;626-644;6
A;Spycher, S.E.; Nick, H.S. 1681, E.E.
                                                                                                                                                                                                                                                                                                                                                                                    R:TOSI, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E. J. Mol. Biol. 208, 709-714, 1989
A;Tille: Complement genes C1r and C1s feature an intronless A;Reference number: S05634; MUID:90040704; PMID:2553984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-688 < KUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A40496; A; Accession: A40496
                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S05634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-688 <MAC>
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A; Residues: 1-688 < TOS>
                                                                                                                                                                                                                                                                                                                                            A; Status: not compared with conceptual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
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Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S26732
                                                                    Nick, H.; Rick11
156, 49-57, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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R; Tosi, M.; Duponchel, C.; Meo, Sinchemistry 26, 8516-8524, 1987
A;Cross-references: GB:M18767; NID:g179647; PIDN:AAA51853.1; PID:g179648 R;Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E. Eur. J. Blochem. 169, 547-553, 1987 A;Title: Molecular cloning of cDNA for human complement component Cls. The A;Reference number: S00224; MUID:88082788; PMID:3500856 A;Accession: S00224
                                                                                                                                                                                                                                                                                A;Title: Complete cDNA sequence of human c
A;Reference number: A27381; MUID:88163522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Jun-2002 C;Accession: A40496; A27381; S00224; S26732; S05634; A05140; A25396; A38407; R;Kusumoto, H.; Hirosawa, S.; Salier, J.P.; Hagen, F.S.; Kurachi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement subcomponent C 1SBAR.GIF (EC 3.4.21.42) precursor N;Alternate names: C1 esterase precursor
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:J04080; NID:g179645; PIDN:AAA51852.1; R;T051, M.; Duponchel, C.; Meo, T.; Julier, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Human genes for complement components Clr and Cls in a close tail-to-tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kusumoto, H.; Hirosawa, S.; Salier, J.P.; Hagen, Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYLLFSSATDQYGPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTY--ASSDHPD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSDNLFTQRTGVITSPDFPNPYPKSSECLYTIELEEGFMVNLQFEDIFDIQDHPEVPCPY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVDCRAPGELEHGLITFSTRNNLTTYKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQPPVHGKIEPSQAKYFFKDQVLVSCDTGYKVLKDNVEMDTFQIECLKDGTWSNKIPTCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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                                                                                                                                                                                                                                                                                   complement C1s
2; PMID:2831944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                    and
                                                              component Cls. The
                                                                                                                                                                                                                                                                                                                 close physical linkage
                                                                                                                                                                                                                                                                                                                                                                                                          PID:g179646
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                                                                 complete
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s C2 and C4
C;Comment: C
C;Genetics:
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F:16-437/Product: complement subcomponent Cls chain A (heavy chain) #status experimental
F:135-171/Domain: EGF homology <EGF>
F:175-887/Domain: Clr/Cls repeat homology <CIR2>
F:294-354/Domain: complement factor H repeat homology <FH1>
F:359-421/Domain: complement factor H repeat homology <FH2>
F:359-421/Domain: complement factor H repeat homology <FH2>
F:438-688/Product: complement subcomponent Cls chain B (11ght chain) #status experimenta
F:438-689/Product: complement subcomponent Cls chain B (11ght chain) #status experimenta
F:438-675/Domain: trypsin homology <TRY>
F:438
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A.Molecule type: protein
A.Residues: 131-134,'X',136-146,'X',148-150;155,'X',157-162;166-170,'X',172-174,'X',176-182,'X',387-402,'X',404-408;416-424,'X',426-431;547-556;592-597;617,'X',619-627,'X',629-635
R.Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
J. Biol. Chem. 265, 14469-14475, 1990
J. Biol. Chem. 265, 14469-14475, 1990
A.Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH.
A.Teles Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH.
A.Reference number: A37820; MUID:90354439; PMID:2387866
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F;11-127/Domain: Cir/Cis repeat homology <CIR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A32672; MUID:90283368; PMID:2141278
A;Contents: annotation; erythro-beta-hydroxyasparagine site, content
A;Note: about half of the A chains contain erythro-beta-hydroxyasparagine
A;Note: This protein is a serine proteinase that combines with Ciq and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule Lype: Fig. 287-293, 'K
A; Residues: 16-61;168-219;287-293, 'K
R; Hess, D.; Schaller, J.; Rickli, E.
R; Hess, D.; 20 2827-2833, 1991
RESULT
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A; Note: the list of introns may be incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 16-25; x', 203-207 <THI>
R; Thielens, N.M.; Van Dorsselaer, A.;
Biochemistry 29, 3570-3578, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 30, 2827-2833, 1991
Biochemistry 30, 2827-2833, 1991
A; Title: Identification of the disulfide bonds of human
A; Reference number: A38407; MUID:91175725; PMID:2007122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 12p13-12p1
A; Introns: 291/1; 329/3; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149/Modified site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimenta: 174,406/Binding site: carbohydrate (Asn) (covalent) #status experimental: 437-438/Cleavage site: Arg-Ile (complement subcomponent Clr) #status experimental: 475,529,632/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2 and C4.
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                                                                                                                                                                                                                                                                                                              DLTGOKKGWKLRYHGDPMPCPKEDTPNSVWEPAKAKYVFRDVVQITCLDGFEVVEGRVGA
                                                                                                                                                                                                                                                                                                                                                                                             GSHISGRGFLLTY-----ASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISG
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C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 30-Jun-1991 #text_change 03-Jun-2002
C;Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
R;Leytus, S.P.; Kurachi, K.; Sakariassen, K.S.; Davie, E.W.
Biochemistry 25, 4855-4863, 1986
                                                                                                          A;Reference number: A29769; MUID:87241248; PMID:3036070 A;Accession: A29769
                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-151, 'L', 153-705 < JOU>
A; Cross-references: GB: X04701; NID: 929538; PIDN: CAA28407.1;
R; Arlaud, G.J.; Willis, A.C.; Gagnon, J.
Biochem. J. 241, 711-720, 1987
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J. Clin. Invest. 98, 2324-2331, 1996
A;Title: Hensin, a new collecting duct protein involved A;Reference number: Z20851; MUID:97096804; PMID:8941650
A;Accession: T30549
                                                                                                                                                                                                                                                                                                                       Biochem. J. 240, 783-787, 1986
A;Title: Cloning and sequencing of full-length cDNA encoding
A;Reference number: A29768; MUID:87156625; PMID:3030286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Nucleotide sequence of the cDNA coding for human complement Clr A; Reference number: A24170; MUID:87026566; PMID:3021205
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A;Cross-references: EMBL:AF043112; NID:g4105083; PID:g4105084; PIDN:AAD02242.1
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C; Accession: T30549
                        R; Arlaud, G.
                                                                      A; Molecule type: protein A; Residues: 18-166, 'X', 168-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-705 <LEY>
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                                           A; Note: 152-Leu was also found
                                                                                                                                                                                                                                                                                                         A; Accession: A29768
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                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M14058; NID:g179643; PIDN:AAA51851.1; PID:g179644
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van Dorsselaer, A.; Bell, 129-134, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 150; DB 2;
Pred. No. 0.0065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
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                     A.; Mancini, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDSWDTQDAQVVCRQLQCGDAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change
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                        Aude,
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                                                                                                                                                                                                                                   PID:g29539
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                                                                                                                                                               complement-classical-pa
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                     C.; Gagnon,
                                                                                                                                                                                                                                                                                                                                                  precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vitro
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Identification of erythro-beta-hydroxyasparagine
nce number: S02422; MUID:88005128; PMID:2820791

in the

EGF-like

domain

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C;Superfamily: complement subcomponent Clr; Clr/Cls rej
C;Superfamily: complement subcomponent Clr; Clr/Cls rej
C;Reywords: acute phase; beta-hydroxyasparagine; calcif
F;1-17/Domain: signal sequence #status predicted <SIG>
F;17-138/Domain: Clr/Cls repeat homology <Clri>Clr/Cls 
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A;Experimental source: plasma
C;Comment: Clr is a dimer of identical chains, each of which is activated by cleavage in
A;Camment: While fragment gamma remains disulfide-bonded to the B chain to form Clr II.
A;Camment: This protein is a serine protease that combines with Clq and Cls to form Cl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; J. Biol. Chem. 265, 14469-14475, 1990
A;Title: Ca(2+) binding properties and Ca(2+)-dependent in A;Reference number: A37820; MUID:90354439; PMID:2387866
A;Accession: A37820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 133-137;187-211;610-613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 18-26; 'L', 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blochemistry 22, 1758-1764,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119729;
A;Map position: 12p13-12p13
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Best I
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;464-705/Product: complement C1r chain B #status experimental <BCH>
;464-67/Domain: trypsin homology <TRY>
;71-89.146-165.161.174.176-189.193-220.250-268.309-358.338-371.376-429.406-447.451-577,
;125,221.514.581/Binding site: carbohydrate (Asn) (covalent) #status experimental
;107/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
;206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experimental
;403-464/Cleavage site: Arg-Ile (autolytic) #status experimental
;502,557,654/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fittle: Complete amino acid sequence of the catalytic chain; Reference number: A00916; MUID:83204782; PMID:6303394

AACCESSION: A00916
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BS Lett. 386, 15-20, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146-189/Domain: EGF homology <EGF>
193-302/Domain: C1r/C1s repeat homology <C1R2>
297-463/Product: C1r gamma fragment #status experimental <
309-371/Domain: complement factor H repeat homology <FH1>
376-447/Domain: complement factor H repeat homology <FH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-463/Product: complement C1r chain  #status experimental <ACH>
146-189/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activate C2 and C4.
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                                                                                                                                                                                                                                                                                                                                                                          PYCGSWAVP------KELRLNSNEVTVLF------KSGSHISGRGFLLTYASSDHPDL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDLNIE-SKTCASDYLLFSSATDQYG 100
                                                                                GCHINLLQ 212
                                                                                                                                                 DECASR-SKSGEEDPQPQCQHLCHNYVGGYFCSCRPGYELQEDRHSCQAECSSELYT-EA
                                                                                                                                                                                                                         ITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGY--RDTSLLCKAAIHAGIITDEL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVTSPLFPKPYPNNFETTTVITVPTGYRVKLVFQQFDLEPSEGCFYDYVKISADKKSLG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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       209
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27.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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Pred. No. 0.00;
30; Mismatches
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jeon, G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 705;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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A; Title: Embryonic expression of mouse bone morphogenetic A; Reference number: I49540; MUID:94229342; PMID:8174772 A; Accession: I49540
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                                                                                                          R; Fukagawa, M.; Noboru, S.;
Dev. Biol. 163, 175-183, 19
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F;33-986/Product: procollagen C-endopeptidase tolloid-like splice form #status pred F;130-321/Domain: astacin homology <AST>
F;32-431/Domain: Clr/Cls repeat homology <ClR2>
F;435-544/Domain: Clr/Cls repeat homology <ClR2>
F;551-587/Domain: Clr/Cls repeat homology <ClR3>
F;591-700/Domain: Clr/Cls repeat homology <ClR3>
F;707-742/Domain: Clr/Cls repeat homology <ClR4>
F;747-856/Domain: Clr/Cls repeat homology <ClR4>
F;747-856/Domain: Clr/Cls repeat homology <ClR4>
F;860-973/Domain: Clr/Cls repeat homology <ClR5>
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,6 F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted F;164/Active site: Glu #status predicted
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A; Residues: 703-986 <TAK>
A; Residues: 6B:L35279;
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A; Molecule type: mRNA
A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRYQKRNRTPQ' <WOZ>
A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRYQKRNRTPQ' <WOZ>
A; Cross references: GB: M22488; NID: 917949; PIDN: AAA51833.1;
R; Takahara, K.; Lyyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
J. Biol. Chem. 269, 32572-32578, 1994
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-200 C;Accession: I49540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homolog C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:BMP1; BMP-1
A;Cross-references: GDB:1
A;Map position: 8p21-8p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitt Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones A; Reference number: A37278; MUID:89072730; PMID:3201241
A; Accession: A37278
                                                                                                                                            149540
                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue A; Reference number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
C; Date: 28-Mar-1998 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              procollagen C-endopeptidase (EC 3.4.24.19)
N;Alternate names: bone morphogenic protein
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Best Local S
Matches 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID: g619860; PIDN: AAC41710.1;
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Hogan,

B.L.M.;

Jones, C.M.

21-Jan-2000

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A;Title: Molecular cloning and characterization of MFRP, a
A;Reference number: JC7629; MUID:21164708; PMID:11263980
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F;556-92/Domāin: EGF homology <EG1>
F;556-92/Domain: C1r/C1s repeat homology <CIR>
F;712-747/Domain: EGF homology <EG2>
F;218-222,228,277/Binding site: zinc (His, His, His, F;218,222,228,277/Binding site: zinc (His, His, His, F)
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A;Residues: 1-579 <KAT>
A;Cross-references: DDBJ:AB055505
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A; Residues: 1-991 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Homo sapiens (man)
Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001;
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Matches
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Best Local :
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LLVPR 527
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                                                                               ELACEPYQYEMCLGLSYNTTAFPNIWYGMITQEEYVEVLSGYKSLTSLPCYQHFRRLLCG 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                   5.3%; Score 142; DB 2; 23.7%; Pred. No. 0.0064;
                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                             --- AGGCKGVQWMCDMWRDCTDGSDDNCSGPLFPPP 462
                                                                                                                      IHAGIITDE-----LGGHINLLQSKGISHYEGLLAN 225
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Search completed: May 15, Job time: 23.454 secs

2003, 13:17:00

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision
C;Accession: T42721
R;Cheng, H.; Bjerknes, M.; Chen, H.
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A;Experimental source: strain BALB/c; jejunal epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: transmembrane protein
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A; Residues: 1-2083 <CHE>
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Best Local
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NETINYSNFLRAVVSN-GII----KRRKDLNIHVSCKMLQNT--WVNTMY 1853
                                                                           --NHMQASVSRSYLQSMGYSARDLVIPGWNSSYHCQPQITQREVIFTIPYTGCGTIKQAD 1810
                                                                                                                                                                                           PDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDE 203
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                                    --AIPSVIFIALLLTGMGIFAICRKRKKKGNPYVSAD-AQKTGCWKQIKY
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| ESULT 1  AS2_HUMAN  D MAS2_HUMAN STANDARD; PRT; 686 AA.  C 000187; 075754; 098270; 0982H0;  T 30-MAY-2000 (Rel. 39, Created)  T 30-MAY-2000 (Rel. 39, Last sequence update)  T 15-UN-2002 (Rel. 41, Last annotation update)  E Mannan-binding lectin serine protease 2 precursor (FC 3 4 21 -) | 105.5 3.9 1493 1 NEOL MOUSE P97798 105.5 3.9 620 1 EXTN_TOBAC P13983 105 3.9 968 1 BCAL RAT 063767 104.5 3.9 570 1 FBP3_STRPU 104.5 3.9 1069 1 ENTK_MOUSE P97435 104.5 3.9 1461 1 NEOL_HUMAN P97435 104 3.9 310 1 ASTL_COTJA P42662  ALIGNMENTS | TSG6_MOUSE 008859 TSG6_HUMAN P98066 FBP1_STRPU P10079 TSG6_RABIT P98065 MSH5_CAEEL 019272                  |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|
|                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                 | 008859 mus musculu<br>p98066 homo sapien<br>p10079 strongyloce<br>p98065 oryctolagus<br>Q19272 caenorhabdi |

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PubMed=10092804;

Stover C.M., Thiel S., Thelen M., Lynch N.J., Vorup-Jensen T.,

Jensenius J.C., Schwaeble W.J.;

"Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single structural gene.";

J. Immunol. 162:3481-3490(1999). Thiel S., Vorup-Jensen T., Stover C.M., Schwaeble W., Laurs Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov [Reid K.B.M., Jensenlus J.C.; "Identification and characterization of a novel protein of complement system, mannan-binding
(MASP-2)."; "A second serine protease associated activates complement."; nature 386:506-510(1997). Thiel S., Jensen T.V., Stover C.M., Some Poulsen K., Willis A.C., Eggleton P., Reid K.B.M., Jensenius J.C.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases SEQUENCE FROM N.A. MEDLINE=97242412; PubMed=9087411; TISSUE-Liver; SEQUENCE FROM N.A. lectin-associated Schwaeble W.J., Laursen S., Hansen S., Holmskov U., with mannan-binding lectin that e W., Laursen Holmskov U., serine AN IMPORTANT ROLE protease-2 the human S.B., S.B.,

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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM000179; EGF_CA; 1.
SMART; SM00020; TryP_SPC; 1.
PROSITE; PS001010; ASX_HVDROXYL; 1
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF_C; 1.
PROSITE; PS01187; EGF_C; 1.
PROSITE; PS01187; EGF_C; 1.
PROSITE; PS0134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00136; TRYPSIN_SER; 1.
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EMBL; X98400; CAA57050.1; -.
EMBL; Y18287; CAB50735.1; -.
EMBL; Y18286; CAB50735.1; -.
EMBL; AF321562; AAG50274.1; -.
EMBL; AF321559; AAG50274.1; JO
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Pfam; PF00089; trypsin; 1.
Pfam; PF00431; CUB; 2.
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iPR000859; CUB_domain.
iPR001314; Chymotrypsin.
iPR000561; EGF-like.
iPR001881; EGF_Ca.
iPR001254; Ser_protease_Try.
iPR000436; Sushi_SCR_CCP.
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CASP_MESAU
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DT 01-APR
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CC EUKATY
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Best Local S
Matches 52
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P15156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete primary structure of calcium-dependent capable of degrading extracellular matrix protein FEBS Lett. 250:411.415(1989).

-1- FUNCTION: CAPABLE OF DEGRADING EXTRACELLULAR CASP DEGRADES TYPE I AND IV COLLAGEN AND FIBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14,
01-APR-1990 (Rel. 14,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinoshita H., Sakiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89325606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sono K., Sakiyama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A., AND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
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                                                                                                                                      PRESENCE OF CALCIUM.

SUBUNIT: HETERODINER, CONSISTING OF HEAVY AND LIGHT CHAINS WITH DISULFIDE BONDS. THE HEAVY CHAIN IS EXPECTED TO BE A REGULATORY SUBUNIT AND THE LIGHT CHAIN CONTAINS THE CATALYTIC SITE.

DOMAIN: THE GLU-RICH REGION IN THE N-TERMINAL REGION MAY BE GAMP.

CARBOXYLATED AND FUNCTION AS A CALCIUM-BINDING SITE.

SIMILARITY: TO BLOOD COAGULATION FACTORS SUCH AS IX, X AND AN ANTICOAGULATION FACTOR, PROTEIN C.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKAAIHAGIITDELGGHINLLQSKGISHYEGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2753140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H., Tokunaga K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW;
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D -> Y (IN REF. 4).
L -> LCS (IN REF. 3).
G -> E (IN REF. 4).
G -> E (IN REF. 4).
MISSING (IN REF. 3).
L -> LIL (IN REF. 3).
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Pred. No. 2.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Imajoh-Ohmi S.,
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Query Match
Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS00022; EGF_1; FALSE_NEG.

PROSITE; PS01186; EGF_2; FALSE_NEG.

PROSITE; PS01186; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Signal;
SIGNAL
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                     126
                                          221
                                                                                    161
                                                               72
                                                                                                15 FAVCAP---LRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRL
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                                                                                    FCSCPPEYFLHDDMRNCGVNCSGNVFTALIGEISSPNYPNPYPENSRCEYQILLEEGFQV
                     GSHISGRGFLLTYASSDHPDLITC---
                                         VVTIQREDFDVEPADSQGNCQDSLLFAAKNRQFGPFCGNGFPGPLTIETHSNTLDIVFQT
                                                               ILRL--GDLNIE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF0043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00084;
                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00032;
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                                                                                                                                         Similarity
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IPR000859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR00131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease; Calcium-binding; Extracellular matrix; oxyglutamic acid; Vitamin K; Hydroxylation; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      email
                                                                                                                                                                                                                                                                                                                                                                           445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sushi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 a license agreement (See http://www.isb-sib.ch/announce/
to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                               695
444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asx_hydroxyl.; CUB_domain.; Chymotrypsin.
                                                             SKTCASDYLLFSSATDQYGPYCGS-WAVPKELRLNSNEVTVLFKS
                                                                                                                                                                         77493
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Sushi_SCR_CCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     like.
                                                                                                                                                                 SERINE PROTEASE.

SERINE PROTEASE.

EGF-LIKE, CALCIUM-BINDING (POTENTIAL).

HYDROXYLATION (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

BY SIMILARITY.

                                                                                                                              37;
                                                                                                                                       Score 158.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                          SUSHI 1.
                                                                                                                                                                                                                                                                                                                                         GLU-RICH
CUB 1.
                                                                                                                                                                                                                                                                                                                                                                CALCIUM-DEPENDENT CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-DEPENDENT CALCIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FALSE_NEG.
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        K; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                      (ACIDIC).
                                                                                                                         J.00015;
76;
                    LERGSHYFEEKYSKFCPAGCRDIAG
                                                                                                                                                                                                                                                                                                                                                                                               SERINE
SERINE
                                                                                                                                                                                                                                                                                                                                                                          SERINE
                                                                                                                              Indels
                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                               PROTEINASE HEAVY
                                                                                                                                                    695;
                                                                                                                              25;
                                                                                                                             Gaps
                    174
                                          280
                                                               125
                                                                                    220
                                                                                                        71
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        InterPro;
InterPro;
                             InterPro;
InterPro;
                                                                                   EMBL;
HSSP;
                                                               MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB,
                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996
01-FEB-1996
                                                    InterPro;
                                                                         MEROPS;
                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASP1 OR CRARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P98064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRAR_MOUSE
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                                                                          S01
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modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no resu
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi A., Takayama Y., Hatsuse H., Kawakami M.; "Presence of a serine protease in the complement-activating component of the complement-dependent bactericidal factor, RaRF, in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-BALB/c; TISSUE-Liver; MEDLINE-94179811; PubMed-8133044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precursor
(EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaKF)
(Mannan-binding lectin serine protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor is a new serine protease
Clr and Cls.";
                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/c; TISSUE-Liver; MEDLINE-93176166; PubMed-8439319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 465-704 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takayama Y., Takada F., Takahashi A., Kawakami M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: COMPONENT OF THE BACTERICIDAL RA-REACTIVE FACTOR RAFF WHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED BY CERTAIN ENTEROBACTERIA. IT TRIGGERS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE C4 COMPONENT BY CLEAVING THE ALPHA-CHAIN OF C4.

SUBUNIT: RARE CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT (CRARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT.

CRARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGH CHAIN (29)
                                                                                                               MGI:88492; Masp1.
rPro; IPR000152; /
                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                 D16492; BAA03944.1; P00736; 1APQ.
                                                                  IPR000859;
IPR001314;
                          IPR001881;
                                                 IPR000561;
  IPR001254;
                                                                                                                                                     .198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                     CUB_domain.
Chymotrypsin.
EGF-like.
EGF_Ca.
Ser_protease_Try.
                                                                                                               Asx_hydroxyl
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                               DOMAINE
ACT_SITE
ACT_
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DOMAIN
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DOMAIN
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     237
                                        369
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                                                                                                             309
                                                                                                                                                                                 250
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                                                                                                                                                                                                                                                                                                                                           Local
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     ×
                                                                                                                                                                                                                                                                        CGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDL-NIESK---TCAS
                                                                                                                                            --PDLITCLE--RGSHYFEEKYSKFCPAGCRDIAGDISGNT-----KDGYRDTSL-LCK
                                                                                                                                                                                                                   DYLLESSATDQYGPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDH----
                                                                                                                                                                                                                                                    CSGNLFTQRTGTITSPDYPNPYPKSSECSYTIDLEEGFMVSLQFEDIFDIEDHPEVPCPY 249
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                                     IVDCGAPAGLKHGLYTFSTRNNLTTYKSE-IRYSCQQPYYKMLHNTTGYYTCSAHGTWTN
                                                                                                         LQPPVYGKIEPSQAVYSFKDQVLVSCDTGYKVLKDNGVMDTFQIECLKDGAWSNKIPTCK
                                                                                                                                                                               DYIKIKAGSKVWGPFCGEKS-PEPISTQTHSVQILFRSDNSGENRGWRLSYRAAGNECPK
     237
                                                                                                                                                                                                                                                                                                                            1 Similarity
58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00032; CCP; 2.
SM00042; CUB; 2.
SM00179; EGF_CA;
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                                                                        AAIHAGIITDELGGHINLLQSKGISH-----YEGLLAN--GV--LSRHGSLSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79895 MW;
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CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
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Pred.
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SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
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70 KDA CHAIN
29 KDA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                           157.5;
No. 0.
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).00019;
hes 93;
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                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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(BY)
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(P29).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Y SIMILARITY).
Y SIMILARITY).
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                                                                                                                                              192
                                                                                                                                                                               308
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PROSITE;
PROSITE;
                                                                                                                                                                               PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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Transmembrane;
Antigen. 1
SIGNAL 1
CCHAIN 22
DOMAIN 861
DOMAIN 861
DOMAIN 87
DOMAIN 87
DOMAIN 147
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01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                         SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS00740; MAM_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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MEDLINE=91337458; PubMed=1908252;

MEDLINE=91337458; PubMed=1908252;

MEDLINE=91337458; PubMed=1908252;

Thakagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;

"The A5 antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors.";

Neuron 7:295-307(1991).

-I- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOU SYSTEM, IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (B SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement or send an email to license@isb-sib.ch
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01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Neuropilin-1 precursor (A5 protein) (A5 antigen).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; (Dordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00629; MAM; 1.
Pfam; PF00754; F5_F8_type_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000859; CUB_domain.
InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; CUB;
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HSSP; P12259;
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NCBI_TaxID=8355;
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PS50060;
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Mol. Immunol. 36:505-514/1000.
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"Exon structure of the gene encodin
protein-associated serine protease
complement Clr and Cls genes.";
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"Molecular characterization of a non
activation of the complement system
int. Immunol. 6:665-669(1994).
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"A new member of the C1s family of complement proteins found bactericidal factor, Ra-reactive factor, in human serum.";
Biochem. Biophys. Res. Commun. 196:1003-1009(1993).
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D17525; BAA04477.1;
D28593; BAA05928.1;
D61695; BAA34864.1;
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SEQUENCE FROM N...
TISSUE-Liver;

MEDLINE-88082788; PubMed=3500856;

MCKinnon C.M., Carter P.E., Smyth S.J.,

M' Molecular cloning of cDNA for human co
complete amino acid sequence.";

complete amino acid sequence.";
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Q9UCV3; Q9UCV4; Q9UCV5;

O1-MAR-1989 (Rel. 10, Created)

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15-JUN-2002 (Rel. 41, Last annotation

Complement C1s component precursor (EC
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MEDLINE-88163522; PubMed-2831944;

Tosi M., Duponchel C., Meo T., Julier

Tomplete cDNA sequence of human compl

linkage of the homologous genes Cls an

Biochemistry 26:8516-8524(1987).
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MEDLINE-91175725; PubMed-2007122;
Hess D., Schaller J., Rickli E.E.;
"Identification of the disulfide bonds of human
Biochemistry 30:2827-2833(1991).
                                                                                                                                                                                                                                                      onset multiple autoimmune diseases.";
J. Immunol. 166:7612-7616(2001).
                                                                                                                                                                                                                                                                                         Dragon-Durey M.-A., Quartier P., Fremeaux-Bacchi V., Blouin de Barace C., Prieur A.-M., Weiss L., Fridman W.-H.; "Molecular basis of a selective C1s deficiency associated wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rossi V., Gaboriaud C., Lacroix M., Gagnon J., Arlaud G.J.;
"Structure of the catalytic region of the study by chemical cross-linking and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91308095; PubMed=1854725; Illy C., Thielens N.M., Gagnon J., Arlaud G.J.; Fielens N.M., Gagnon J., Arlaud G.J.; Effect of lactoperoxidase-catalyzed iodination on the Ca(2+)-dependent interactions of human Cls. Location of the iodination
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MEDLINE-84104122; PubMed-6362661;
Carter P.E., Dunbar B., Fothergill J.E.;
"The serine proteinase chain of human co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human complement component Cls. Partial sequence the heavy chain and identification of the peptide
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IMMUNOI. 166:7612-7616(2001).

IMMUNOI. 166:7612-7616(2001).

FUNCTION: C1S B CHAIN IS A SERINE PROTEASE THAT COMBINES WITH C1Q AND C1S TO FORM C1, THE FIRST COMPONENT OF THE CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. C1R ACTIVATES C1S SO THAT IT CAN, IN TURN, ACTIVATE C2 AND C4.

CATALYTIC ACTIVITY: CLEAVES COMPONENT C4 TO C4A AND C4B, AND CAMPONENT C2 TO C2A AND C2B.

SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1O, R AND S IN THE MOLAR RATION OF 1:2:2. ACTIVATED C1S IS AN DISULFIDE-LINKED HETERODIMER OF AN HEAVY CHAIN AND A LIGHT CHAIN.

DISEASE: Defects in C1S are the cause of selective C1s deficiency, that is associated with early onset multiple autoimmune diseases.
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ement genes Clr and Cls feature an
closely related to haptoglobin.";
. Biol. 208:709-714(1989).
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CUB 1. EGF-LIKE, CUB 2. SUSHI 1. SUSHI 2.

CALCIUM-BINDING (POTENTIAL)

SERINE

N-LINKED

HYDROXYLATION (PROBABLE)
N-LINKED (GLCNAC. . .).

(GLCNAC. . .).

E RELAY SYSTEM.
E RELAY SYSTEM. PROTEASE COMPLEMENT

C1S

HEAVY LIGHT

CHAIN

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SMART; SM0003
SMART; SM0004
SMART; SM0017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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PIR; S00224; S00224.
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PF00431;
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PS01186;
PS01187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50240; TRYPSIN_DOM;
PS00134; TRYPSIN_HIS;
PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000152;
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247; C1S.
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); ASX_HYDROXYL;
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EGF_1; F
EGF_2; F
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RYPSIN_SEN, -.
Plasma; Glycoprotein; Serin
Plasma; Signal; EGF-like
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RESULT 7
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Best Local
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21-JUL-1986
01-AUG-1988
15-JUN-2002
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  "Complete amino acid sequence of complement subcomponent C1-r.", Biochemistry 22:1758-1764(1983).
                                                                                      SEQUENCE OF 18-463.

MEDLINE-87241248; PubMed-3036070;

Arlaud G.J., Willis A.C., Gagnon J.;

"Complete amino acid sequence of the
classical-pathway enzyme Clr.";

Biochem. J. 241:711-720(1987).
                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Complement Clr component precursor (EC 3.4.
                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-87156625;
                                                                                                                                                                                                                                            Leytus S.P., Kurachi K., Sakariassen K.s
"Nucleotide sequence of the cDNA coding
Biochemistry 25:4855-4863(1986).
                                             MEDLINE-83204782;
Arlaud G.J., Gagno
                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-87026566;
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                                                                    SEQUENCE OF 464-705.
                                                                                                                                                                                         "Cloning
                                                                                                                                                                                                    Journet A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335
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                                                                                                                                                                             complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                    and sequencing of full-length mplement component C1r.";
J. 240:783-787(1986).
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386
425
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628
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513
573
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                                             Gagnon
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                                                         PubMed=6303394;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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-> A (IN REF. 7).
X -> GR (IN REF. 7).
85522647A4C47205 CRC64;
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                                     the
                                   catalytic
                                                                                                               A chain
                                                                                                                                                                                                                                                                     K.S.,
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.00058;
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                                                                                                                                                                                                                                                                                                                         Hominidae;
                                                                                                                                                                                                                                                                     Davie
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5).
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                                                                                                                                                                                                                                                        complement C1r.
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                                    of human
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                                                                                                              complement-
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Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF00431; CUB; 2.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00179; EGF_CA; 1.
SMART; SM0010; ASX_HYDROXYL; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                            InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
InterPro; IPR001861; EGF_da.
InterPro; IPR001254; Ser_protease_Tr;
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                             EMBL; X04701; CAA28407.1;
EMBL; M14058; AAA51851.1;
PIR; A24170; CTHURB
PDB; 1APQ; 17-SEP-97.
MEROPS; S01.192; -
                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                              This
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MEDLINE-96221263;
                                                                                                                                                                                                                         Genew; HGNC:
MIM; 216950;
                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in human complement interaction.";
                                                                                                                                                                                                                                    HGNC:1246; C1R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 133-137;
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Biochemistry 37:1204-1214(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of erythro-beta-hydroxyasparagine domain of human Clr.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bersch B., Hernandez J.-F., Marion D., "Solution structure of the epidermal g
                                                                                                                                                     -I- CATALYTIC ACTIVITY: ACTIVATES C1S BY PROTEOLYTIC CITHAT IT CAN, IN TURN, ACTIVATES C2 AND C4.

- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR CON AND S IN THE MOLAR RATION OF 1:2:2. C1R IS A DIMER CHAINS, EACH OF WHICH IS ACTIVATED BY CLEAVAGE INTO AND B, CONNECTED BY DISCULFIDE BONDS.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Identification of a cryptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    human complement protease Clr,
                                                                          s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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PubMed=8635594;
ens N.M., Hudry-Clergeon
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                    http://www.isb-sib.ch/announce/
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PROSITE; PS00135; TRYPSIN_SER; 1.
Complement pathway; Plasma; Glycoprotein; Serine protease; Hydrolase;
Hydroxylation; Phosphorylation; Sushi; Repeat; Signal;
                                              Cochlin precursor COCH OR COCH582.
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Mammalia; Eutheria;
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39, Last sequence up
41, Last annotation
                                                            (COCH-5B2).
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Primates;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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Craniata; Vo
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GLCNAC. .).
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                Vertebrata; Euteleostomi;
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VARIANTS DFNA9 GLY-66; GLU-88 AND ARG-117.

MEDLINB=99021390; PubMed=9806553;

ROBERTSON N.G., Lu L., Heller S., Merchant S.N., Eavey R.D.,

MCKenna M., Nadol J.B. Jr., Miyamoto R.T., Linthicum F.H. Jr.,

Meto J.F.L., Hudspeth A.J., Seidman C.E., Morton C.C., Seidman J.G.;

"Mutations in a novel cochlear gene cause DFNA9, a human nonsyndromic deafness with vestibular dysfunction.";

Nat. Genet. 20:299-303(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Genetic studies of a family with inherited domi
Unpublished observations (JAN-2000).
-: SUBCELLULAR LOCATION: Secreted (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Kok Y.J.M., Bom S.J.H., Brunt T.M., Kemperman M.H., van Beusekom E., van der Velde-Visser S.D., Robertson Morton C.C., Huygen P.L.M., Verhagen W.I.M., Brunner H.Cremers C.W.R.J., Cremers F.P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robertson N.G., Skvorak A.B., Kovatch K.A., Battey J.F., Bie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vestibular defects."
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AND THE VESTIBULE.

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AND THE VESTIBULE.
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                                                                                                                                                                                                                                                                                                                                                                       WWW="http://www.expasy.org/spotlight/articles/sptlt004.html"
DATABASE: NAME=Hereditary hearing loss homepage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NONSYNDROMIC SENSORINEURAL DEAFNESS TYPE 9 (DFNA9). AFFECTED INDIVIDUALS HAVE MUCOPOLYSACCHARIDE DEPOSITIONS IN THE CHANNELS THE COCHLEAR AND VESTIBULAR NERVES. THESE DEPOSITIONS APPARENTLY
                                                                                                                                                                                                                                                                                                                                          WWW="http://www.uia.ac.be/dnalab/hhh/hhhgenes.html".
                                                                                                                                                                                                                                                                                                                                                        NOTE=Gene page;
                                                                                                                                                                                                                                                                                                                                                                                                         NOTE-Issue 4 of November 2000;
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PRINTS; PR00453; VWFADON SMART; SM00327; VWA; 2. PROSITE; PS50820; LCCL; PROSITE; PS50234; VWFA; between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Us Glycoprotein; EMBL; AF006740; AAC39545.1; HSSP; P11215; LJLM. Pfam; PF00092; InterPro; IPR004043; InterPro; IPR002035; Genew; or send entities requires a license agreement This SWISS-PROT entry is copyright. It is produced through 601369; HGNC: 2180; an email to license@isb-sib.ch). Repeat; vwa; VWFADOMAIN. VWF\_A. Signal; 2: Disease mutation; (See http://www.isb-sib.ch/announce, There are no restrictions ng as its content is in Usage Deafness; and the and EMBL ø for collaboration outstation 8 on way

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RESULT
NRP1_MC
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
"Developmentally regulated expression of a cell surface protein, neuropilin, in the mouse nervous system.";
J. Neurobiol. 29:1-17(1996).

-I- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
                                                                                                             SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Embryonic |
MEDLINE-96353149; PubMed-8748368
                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                      MOUSE
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                              Neuropilin-1
NRP1 OR NRP.
                                                                                                                                                                                                                                                 NRP1_MOUSE
P97333;
                                                                                                     Kawakami A., Kitsukawa T.,
                                                                                                                                                      NCBI_TaxID=10090;
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Rodentia;
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annotation update)
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T -> S (IN DBSNP:
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PROSITE; PS01285; FA58C_1;
PROSITE; PS01286; FA58C_2;
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SMART; SM00231; FA58C;
SMART; SM00137; MAM; 1.
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InterPro; IPR000421;
InterPro; IPR000998;
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: NERVOUS SYSTEM.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 FS/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 2 FS/8 TYPE C DOMAINS.
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 AKEGFSANYSVLQSSISEDF
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Dev. Biol. 163:175-183(1994).

-i- FUNCTION: CLEAVES THE C-TERMINAL PROPERTIDES OF PROCOLLAGEN I, AND II. INDUCES CARTILAGE AND BONE FORMATION.

-i- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at the C-terminal propertide at the C-terminal properties at the C-terminal
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein)
                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
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Fukagawa M., Hogan B.L.M., Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6; TISSUE-Embryo; MEDLINE-94229342; PubMed-8174772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-C57BL/6; TJ
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Mammalia; Eutheria;
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P98063;
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                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: ACTIVITY IS INCREASED BY THE ENDOPEPTIDASE ENHANCER PROTEIN.

TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC AND FLOOR PLAYE REGION OF THE NEURAL TUBE. LESS MEMBRANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF I OF SKIN AND THE MESSNCHYME OF SPLEEN AND LUNG. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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ENZYME REGULATION: ACTIVITY IS INCREASED BY
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PROSITE; PS00010; ASX_HYDROXYL; ;
PROSITE; PS000022; EGF_1; FALSE_NI
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
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ZnMc; 1.
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864
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33.0%;
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EGF-like.
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                                                                                                                                                                                                                                                                              MW;
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BY SIMILARITY.
LINC (CATALYTIC) (BY
ZINC (CATALYTIC) (BY
ZINC (CATALYTIC) (BY
BY SIMILARITY.
BY SIMILARIT
                                                                                                                                                                                 Score 142.5;
Pred. No. 0.00
22; Mismatches
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CUB 3.
EGF-LIKE 2,
CUB 4.
CUB 5.
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CUB 1.
CUB 2.
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68A1847783A0BB9E
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.0044;
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RESULT 11

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BMP1_HUMAN STANDAKU;
BMP1_HUMAN STANDAKU;
BMP1_HUMAN STANDAKU;
Q99422; Q99423; Q148/4
Q1-AN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.
Bone morphogenetic protein (PCP) (Mammalian t
                                                                        the
                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Janitz M., Heiser V., Boettcher U., La
"Three alternatively spliced variants
bone morphogenetic protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Novel regulators of bone formation: activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is identical to the protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM BMP1-3). TISSUE-Skin;
                                               use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95096114; PubMed-7798260;
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science
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MEDLINE-89072730; PubMed-3201241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98160316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The C-proteinase that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96209868;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mol.
                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                          COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
ENZYME REGULATION: ACTIVITY IS INCREASED BY
ENDOPEDIDASE ENHANCER PROTEIN.
ALTERNATIVE PRODUCTS: 7 isoforms; BMP1-1, BM
here), BMP1-4, BMP1-5, BMP1-6 and BMP1-7; ar
alternative splicing.
TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                               AND II. INDUCES CARTILAGE AND BONE FORMATION. CATALYTIC ACTIVITY: Cleavage of the C-terminal Ala-|-Asp in type I and II procollagens and at
                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                        SIMILARITY:
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                               76:141-146(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9500680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORMS BMP1-4;
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                                                          institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        previously identified
                                   agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93:5127-5130(1996).
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                                               removed.
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n tolloid protein) (mTld).
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Arg-|-Asp :
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EMBL; M22488; AAA51833.1
EMBL; Y08723; CAA69973.1
EMBL; Y08724; CAA69974.1
EMBL; Y08725; CAA69975.1
EMBL; L35278; AAC41703.1
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PIR; A37278; A
HSSP; P00736;
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SMART; SM00042; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
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InterPro; IPR000859;
InterPro; IPR000561;
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; PS00142; Zin, 5
E; PS01180; CUB; 5
FE; PS00010; ASX_H
~~00022; EGF
EGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; EGF_CA; 2.
Cytokine; Repeat; Bone; Cartilage; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like domain; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASX_HYDROXYL; 2.
EGF_1; FALSE_NEG.
EGF_2; 2.
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EGF-like.
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                                                  N-LINKED (GLCNAC. ...) (POTENTIAL).
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N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
DKDECSKDNGGCQDCVNTFGSYECQCR -> EKRPALQPP RGRPHGLKFRVQKNARTPQ (IN ISOFORM BMP1-1).
MISSING (IN ISOFORM BMP1-1).
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CUB 5.

ZINC (CATALYTI
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QEYNFLKMEPQEVESLGETYDFDSIMHYARNTFSRGIFLDT
IVPKYEVNGYKEPIGQR -> VLHSSLLLLSGSSRNGASFP
CSLESSTHQALCWTGLELLRPSPFPRLPLAAPRTLRAGV
(IN ISOFORM BMP1-4).
MISSING (IN ISOFORM BMP1-4).
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email to

license@isb-sib.ch).

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RESULT
UVS2_XI
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Best Local
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the Euro
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                                                                                                                                                             SEQUENCE OF 196-514 FROM N.A. MEDLINE=90108413; PubMed=1688538; Sato S.M., Sargent T.D.;
                                                                                                                                                                                                              "Molecular cloning expression in hatch
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-97228908;
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
                                                                                                                                                                                                                                                                                                                       UVS2_XENLA STANDARD; PRT; 514 AA.
P42664;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Embryonic protein UVS. Perceursor (EC 3.4.24.-).
Xenopus laevis (African clawed frog).
                                                     This
                                                                                                                                           Dev
                                                                                                                                                                                                                                  Katagiri C., Maeda
Yasumasu S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                     "Molecular
                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
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                                                           . Biol. 137:135-141(1990).

COPACTOR: BLADS 1 ZINC ION (BY SIMILARITY).

DEVELOPMENTAL STAGE: EXCLUSIVELY IN THE ANTERIOR NEURULA STAGE EMERYOS. BY THE TAILBUD STAGE, THE LOCALIZED IN SPECIALIZED CEPHALIC ECTODERM, IN A CORRESPONDING TO THE HATCHING GLAND.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                              s SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
                                                                                                                                                                                                  ecular cloning of Xenopus hatching ession in hatching gland cells."; J. Dev. Biol. 41:19-25(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLFSSATDQYGP----YCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCDHKVTS-TSGTITSPNWPDKYPSKKECTWAISSTPGHRVKLTFMEMDIESQPECAYDH
                                                                                                                                                                                                                                                                                                                                                                                                                                   LEVFDGRDAKAPVLGRFCGS-KKPEPVLATGSRMFLRFYSDNSVQRKGFQASHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
38; Conserv
             non-profit
and this st
                                                                                                                                         approach to dorsoanterior development 137:135-141(1990).
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                                                                                                                                                                                                                                                                                            Xenopus.
                                                                                                                                                                                                                                                     PubMed=9074934;
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717
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            ormatics Institute. There are no rest
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tatement is not removed. Usage by ar
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                                                                                                                                                                                                                                            Yamashika
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                                                                                                                                                                                                                                                                                                      Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141.5;
Pred. No. 0.00
22; Mismatches
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MISSING (IN ISOFORM BMP1-7).
D -> N (IN REF. 4).
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MISSING (IN ISOFORM BMP1-6).
DKDECSKDNGGCQQDCVNTFGSYECQCRSGFVLHDNKHDCK
                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQEGSYLDFWDTHRGDPKPRRRKSLKTFSLTPATFRG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THAHTHTHVHTHCPIAQETCRGPPLGASRLSPQGPGHLTLA
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VKLTFMEMDIESQPECAYDHLEVFDGRDAKAPVLGRFCG
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DLQVCKPLLWDHCFRLSTHGPEMLGTALRG (IN
ISOFORM BMP1-5).
MISSING (IN ISOFORM BMP1-5).
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                                          It is produced through a collaboration -
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   (See
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   http://www.
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           Usage
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                                         and the
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                                                                                                                                                   in Xenopus laevis.";
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REGION P
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Best Local
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CARBOHYD
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SEQUENCE
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01-FEB-1996
01-FEB-1996
16-OCT-2001
-i- DEVELOPMENTAL STAGE: EMBRYO; HIGHEST LE
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY:
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                              Hwang S.P.L., Partin J.S., Lennarz W.J. "Characterization of a homolog of humar in the embryo of the sea urchin, Strong Development 120:559-568(1994).
                                                                                                                                                                                                                       Bone morphogenetic protein 1 homolog precursor (E
Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000130; Zn_MT Pfam; PF00431; CUB; 2. Pfam; PF01400; Astacin; 1. PRINTS; PR00480; ASTACIN.
                                                                                                                                               TISSUE-Embryo;
                                                                                                                                                                                                Echinoidea; Euechinoidea; Strongylocentrotus.
                                                                                                                                MEDLINE-94215496; PubMed-8162855;
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    BMPH_STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00142; ZINC_
PROSITE; PS01180; CUB;
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InterPro; IPR000130;
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                                                                                                                                                                                  NCBI_TaxID=7668;
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                                                     HATCHED BLASTULA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGAFYSSPK-TFTSPNYPGNYTTNTNCTWTITAPAGFKVSLRITDFELEIGASCRYDYL
                                                                                                                                                                                                                                                                                                                                                                                   NIYNSTLGAVMGPYCGPIDFHSAIVSKSNSMMITMNSDFSKQYKGFSATY
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M27162;
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SM00235; ZnMC; :
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33, Last sequence
40, Last annotation
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400
513
186
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421
                                                                                 J.S., Lennarz W.J.;
a homolog of human bone morphogenetic protein
a homolog of strongylocentrotus purpuratus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.5%;
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                                                                                                                                                                                                            Echinacea;
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1 homolog p
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Pred. No. 0.
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BY SIMILARITY
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                                                                                                                                                                                                            Echinoida; Strongylocentrotidae
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                                                                 PRIMARY
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57;
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C
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.) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                        SPICULOGENESIS
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Best Local
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SMART; SM00179; ESF_CA; 1.

SMART; SM00235; ZDMC; 1.

PROSITE; PS00142; ZINC_PROTE
PROSITE; PS01180; CUB; 2.

PROSITE; PS00010; ASX_HYDRO;
PROSITE; PS00010; ASX_HYDRO;
PROSITE; PS00027; ESF_1; FAI
PROSITE; PS01186; EGF_CA; 1.

PROSITE; PS01187; EFF_CA; 1.
                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
CARBOHYD
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SEQUENCE
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METAL
ACT_SIT
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DOMAIN
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PROPEP
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Pfam; PF00431; CUB; 2.
Pfam; PF01400; Astacin; 1.
PRINTS; PR00480; ASTACIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000561;
InterPro; IPR001881;
InterPro; IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001506;
InterPro; IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L23838; AAA30081.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                             148
                                                                                  480
                                                                                                                           422
                                                                                                       92
                                                                                                                                            33 GHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDLNIE-SKTCASDYLL
                                                                                                                                                                                                                                                                                                                        _SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCLERGSHYFEEKYSKFCP--AGCRDIAGDISGN---
                                                                                                                          GHI--ERESGTLQSPNYPDDYHPSKECVWLITMPANYTVGLSFQSFEIERHETCIYDYVE 479
                                                                                  VRDGHEDTSPLIGRYCG-YFIPDDIKSTGNKMMVTFVSDGSVNKGGF----
                                                                                                     FSSATDQYGP----YCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDHPDLI
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000859;
                                                                                                                                                                                                             455
639
                  IHAGI
                                                                                                                                                                    Conservative
                                        -FFKEKDECAQPDQGGCMDVCVNTIGSYRCDCRPGYELSSDGRR-----CEVA
                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                                                                                                                                                                               8
                  199
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; CUB; 2.
; ASX_HYDROXYL; 1.
; EGF_1; FALSE_NEG.
; EGF_2; 1.
; EGF_CA; 1.
                                                                                                                                                                                                                                   Astacin.
Asx_hydroxyl.
CUB_domain.
EGF-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; Repeat; Hydrolase; Protease; like domain; Calcium; Signal.
                                                                                                                                                                             . 3%;
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                                                                                                                                                                                                         EGF-LIKE, CALCIUM-BINDING (POTENTIAL).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

                                                                                                                                                                     28;
                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                   METALLOPROTEASE.
CUB 1.
CUB 2.
                                                                                                                                                                                                                                                                                                                                                                                     BONE
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   MORPHOGENETIC
                                                                                                                                                                              No. 0.
                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.isb-sib.ch/announce/
                                                                                                                                                                    63;
                                                                                                                                                                                       Length 639;
                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN
                                                            -- TKDGYRDTSLLCKAA
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc;
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                                                                                                                                                                                                                                                                                                                                                                                    1 HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                            Embryo;
                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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                                                                                                                                                                   Gaps
                                       575
                                                            194
                                                                                                                                              91
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REAL DESCRIPTION OF THE PROPERTY OF THE PROPER

EMBL; AF016506; AAD01598.1; InterPro; IPR000859; CUB\_do; InterPro; IPR001134; Netrin

CUB\_domain. Netrin\_C.

CUB;

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MEDLINE-91076903; PubMed-2256940;

Kessler E., Mould A.P., Hulmes D.J.S.;

Procollagen type I C-proteinase enhancer is a national connective tissue glycoprotein.";

Biochem. Biophys. Res. Commun. 173:81-86(1990).

Biochem. Biophys. Res. Commun. 173:81-86(1990).

PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEIN PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINS SECRET.

--- TISSUE SPECIALY TENDON. ALSO EXPRESSED INTESUES, ESPECIALY TENDON. ALSO EXPRESSED INTESUES.
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30-MAY-2000
30-MAY-2000
15-JUN-2002
  EMBL;
EMBL;
EMBL;
                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogata I., Auster A.S., Matsul A., Greenwel P., Geerts A., I Fujiwara K., Kessler E., Rojkind M.; "Up:regulation of type I procollagen C-proteinase enhancer messenger RNA in rats with CCl4-induced liver fibrosis."; Hepatology 26:611-617(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masuda M., Igarashi H., Kano M., Yoshikura H.;
"Proviral integration into the procollagen C-proteinase enhancer
protein gene and its effects in cultured rat fibroblasts revealed
an excisable 'hit and-run' retroviral vector.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Fischer 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Wistar;
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15-JUN-2002 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COH-terminal proteinase enhancer) (Type 1 procollagen
                                                                                                                                           entities
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Morisaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                                                                                                 send
                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collai ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in by non-profit institutions as long as its content is in
U94710; AAB93478.1; -. AB008534; BAA23217.1; -. AF016503; AAD01592.1; -. AF016508; AAD01598.1; -.
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                                                                                                                 an email to license@isb-sib.ch).
                                                                                                                                        requires a license agreement
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Saito Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Aorta;
youfuda K., Harada
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Rodentia;
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21:662-662(1996).
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C-PROTEINASE !
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L outstation -
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RESULT 15
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Best Local S
Matches 70
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TOLLOID OR TLD OR MEN.
Brachydanio rerio (Zebrafish) (
Eukaryota; Metazoa; Chordata; C
Actinopterygii; Neopterygii; Te
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                           TISSUE=Gastrula;
MEDLINE=98057457; PubMed=9395394;
Blader P., Rastegar S., Fischer N., Strael
"Cleavage of the BMP-4 antagonist chordin
Science 278:1937-1940(1997).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
  Development 126:3119-3130(1999).

-I- FUNCTION: Required for patterning ventral increase bone morphogenetic protein (BMF) gastrulation by proteolytic cleavage of ch from inactive complexes.

-I- TISSUE SPECIFICITY: During gastrulation, a
                                                                              FUNCTION, AND TISSUE SPECIFICITY,
MEDIINE-99307076; PubMed-10375503;
Connors S.A., Trout J., Ekker M., J
"The role of tolloid/mini fin in do
                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Greaten,
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                           SEQUENCE FROM N.A.,
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16-0CT-2001
                                                                     zebrafish embryo."
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21.9%;
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PROCOLLAGEN C-PROTEINASE ENHANCER
PROTEIN.

CUB 1.

CUB 2.

NTR.

N-LINED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                      n) (Danio rer
n; Craniata;
Teleostei;
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Pred. No. 0.0
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hordin by zebrafish Tolloid.";
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ta; Vertebrata; Euteleostomi;
ei; Ostariophysi; Cypriniform
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     PROSITE; PS00010; A
PROSITE; PS001180; C
PROSITE; PS00022; E
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SMART; SM00235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; M12.016; -.
ZFIN; ZDB-GENE-990415-265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement
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InterPro; IPR000561;
InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                     METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed in the hematopoietic system.
SIMILARITY: BELONGS TO PERTIDASE FAMILY M12A.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                closing blastopore with greater expression ventrally. At t animal pole, expressed in the ectoderm flanking the anteri neural plate. At the 10-somite stage, expressed in the deviatibud and cranial neural crest. At the 20-somite stage,
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PF00431; CUB; 5.
PF01400; Astacin; 1.
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EGF_CA; 2.
ZINC_PROTEASE;
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EGF_1; FALSE_NEG.
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Q9D696
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| 5.4      | 5.4                | 5.4                | 5.4    | 5.4    | 5.4    |                    |        | 5.6     | 5.7    | 5.7    | 5.7    | 5.7                | 5.8    | 5.8    | 5.9    | 5.9    | 5.9    | 6.0    | 6.0    | 6.0    | 6.0                | 6.1    | 6.1      | 6.2    | 6.2                | 6.2                | 6.2    | 6.3                |
| 579      | 977                | 650                | 722    | 693    | 494    | 1015               | 926    | 1594    | 936    | 919    | 719    | 728                | 745    | 251    | 384    | 276    | 3620   | 746    | 733    | 701    | 685                | 685    | 3623     | 678    | 643                | 623                | 541    | 3623               |
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| Q96DQ9   | Q91925             | Q8VHI5             | Q9PSZ5 | Q96DM8 | 096106 | Q9Y6L7             | Q9UQ00 | Q95218  | QBUVQ9 | Q8UVR0 | Q9PVY2 | Q96RS4             | Q9PVY3 | Q9D9K5 | Q9W630 | Q9BRH3 | Q9TU53 | 001654 | Q920S0 | Q9JJS9 | Q91WP0             | Q9Z338 | 060494   | Q9JJS8 | Q9QX84             | Q9ллР3             | Q9QX90 | 070244             |
| homo sap | Q91925 xenopus lae | Q8vhi5 mus musculu | lamı   | homo   | homo   | Q9y617 homo sapien |        | oryctol | gallus | gallus | triaki | Q96rs4 homo sapien |        |        | 0      |        |        |        | 0      | rati   | Q91wp0 mus musculu | mus    | homo sap | rattus | Q9qx84 rattus norv | Q9jjp3 rattus norv |        | 070244 rattus norv |

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## ALIGNMENTS

RESULT 1 Q9D4J3

| "Functional annotation of a full-length mouse cDNA collection."; nature 409:885-690(2001)1-SIMILARITY: CONTAINS 1 CUB DOMAIN. EMBL: AKO16485: HAR30265 1 | DR  |
|----------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| otation of a full-length mouse cDNA 690(2001).                                                                                                           |     |
| otation of a full-length mouse cDNA                                                                                                                      | 3 6 |
| otation of a full-longth mouse only                                                                                                                      | 2 2 |
| Hayasnızakı Y.;                                                                                                                                          | 3 5 |
| Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki :                                                                                         | R   |
| Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming                                                                                       | RA  |
| Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF                                                                                        | RA  |
| Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,                                                                                             | RS. |
| Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,                                                                                        | RA. |
| Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,                                                                                      | RA  |
| Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,                                                                                          | R.A |
| Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,                                                                                         | RA  |
| Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,                                                                                         | R.A |
| Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio                                                                                        | RA  |
| Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush                                                                                        | Ŗ,  |
| Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,                                                                                           | RA  |
| rner M., Batalov S., Casavant T.,                                                                                                                        | RA  |
| Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito                                                                                                     | RΑ  |
| ., Yamanaka                                                                                                                                              | RΑ  |
| Konno H., Adachi J., Fukuda                                                                                                                              | ₽   |
| Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,                                                                                       | RΑ  |
| MEDLINE=21085660; PubMed=11217851;                                                                                                                       | 2   |
| STRAIN=C57BL/6J; TISSUE=TESTIS;                                                                                                                          | RC  |
| SEQUENCE FROM N.A.                                                                                                                                       | RP  |
| [1]                                                                                                                                                      | RN  |
| NCBI_TaxID=10090;                                                                                                                                        | ×   |
| Rodentia; Sciurognathi; Muridae;                                                                                                                         | 8   |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                                                        | გ   |
| Mus musculus (Mouse).                                                                                                                                    | SO  |
| 4631413K11RIK.                                                                                                                                           | GZ  |
| ik protein.                                                                                                                                              | DE  |
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| Q9D4J3 PRELIMINARY; PRT; 503 AA.                                                                                                                         | Đ   |

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STRAIN-C57BL/GJ; TISSUE-SKIN;

MEDLING-21085660; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Shibata K., Konno H., Adachi J., Pukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Eleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbu
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01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
4631413K11R1k protein.
                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                        SEQUENCE FROM N.A.
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InterPro; IPR000859; CUB_domai
InterPro; IPR0004043; LCCL_dom,
Pfam; PF00431; CUB; 1.
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503 AA; 54547 MW;
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59; CUB_domain.
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RESULT
Q8R327
    RN OCC OF DATE
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence upda
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation upo
DE Similar to RIKEN cDNA 4631413K11 gene.

S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebra
C Bukaryota; Metazoa; Chordata; Sciurognathi. "
NCBI_TaxID=10090;
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-i-SIMILARITY: CONTAINS 1 CUB DEMBL; AK014521; BAB29409.1; ...
MGD: MGI:1913936; 4631413K11Rik.
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SMART; SM00042; CUB; 1.
PROSITE; PS01180; CUB; 1.
SEQUENCE 460 AA; 50334 MW;
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runo M., Aono H., Baldarelli R., Barsh
Bojunga N., Carninci P., de Bonaldo M.F.
C., Fletcher C., Fujita M., Gariboldi M.
C., Hofmann M., Hume D.A., Kanlya M., Lee
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Pred. No. 5.1e-201;
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                            Muridae;
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                                      Euteleostomi;
                           Murinae;
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Lee N.H.,
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Q96PD2;
01-DEC-2001
01-DEC-2001
01-JUN-2002
Endothelial
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Strausberg R.;

Strausberg R.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC026771; AAH26771.1; -.

SEQUENCE 432 AA; 46798 MW; AD3FB42B24CD4917 CRC64;

SEQUENCE 432 AA; 46798 MW; AD3FB42B24CD4917 CRC64;
                                  SEQUENCE FROM N.A.

PubMed-11447234;

Kobuke K., Furukawa Y., Sugai M., Tanigaki K., Oh

Matsumori A., Sasayama S., Honjo T., Tashiro K.;

"ESDN, a Novel Neuropilin-like Membrane Protein C

cells with the Longest Secretory Signal Sequence

Up-regulated after Vascular Injury.";

J. Biol. Chem. 276:34105-34114(2001).

-i- SIMILARITY: BELONGS TO THE CRP/FNR FAMILY OF
                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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[1]
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                       REGULATORS
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(TremBLrel. 19, Last sequence update)
(TremBLrel. 21, Last annotation update)
and smooth muscle cell-derived neuropil
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AAL30178.1;
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Catarrhini;
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Eukaryotes,
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Q8TDX2; Q8TDX2; Q1-JUN-2002 Q1-JUN-2002 Q1-JUN-2002

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

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Last sequence upon Last annotation upon Last annota

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Best Local Similarity
Matches 183; Conserv
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InterPro; IPR000421; FA58_C.
InterPro; IPR0004043; LCCL_dom.
Pfam; PF00431; CUB; 1.
Pfam; PF00754; F5_F8_type_C; 1
PROSITE; PS01180; CUB; 1.
DNA-binding; Transcription reg
SEQUENCE 775 AA; 85034 MW;
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MW; 3D06F81EF2337010 CRC64;
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Pred. No. 2.4e
84; Mismatches
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Best Local Similarity 24.5%;
Matches 183; Conservative 8
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Koshikawa K., Osada H., Kozaki K., Konishi H., Masuda A.,
Koshikawa K., Mitsudomi T., Nakao A., Takahashi T.;
Tatematsu Y., Mitsudomi T., Nakao A., Takahashi T.;
"Significant up-regulation of a novel gene, CLCP1, in a highly
"significant up-regulation of a novel gene, CLCP1, in a highly
"significant up-regulation of a novel gene, CLCP1, in a highly
"oncogene 0:0:0-0(2002).
Oncogene 0:0:0-0(2002).
EMBL; AB073146; BAB91138.1; -.
EMBL; AB073146; BAB91138.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PGLPAPDELVYQVPQSTQEVSGAGRDG
                                                                                                                                    FRPMDTDTEEVRVNTEASGH----YDCPHRPGRHEYALPLTHSEPEYATPIVERHLLRA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                 YQWLQIDLNKEKKITGIITTGSTMVEHNYYVSAYRILYSDDGQKWTVYREPGVEQDKIFQ 407
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                                                                                       HTFSTQSGYRVPG-PRPTHKHSHSSGGFPPATGATQVESYQRPASPKPVGGGYDKP-AAS 462
                                                                                                                                                                                  PAKAVDHEETPVRYSSSE---VNHLSPREVT---TVLQADSAEYAQPLVGGIVGTLHQRST
                                                                                                                                                                                                                                                                           AIPSVI--FIALLLIGMGIFAIC-----RKRKKKGN---PYVSADAQKTGCWKQIKYPF 300
                                                                                                                                                                                                                                                                                                          NSNDLKNTTAPPKIAKGRAPKFTQPLQPRSSNEFPAQTEQTTASPDIRNTTVTPNVTKDV 527
                                                                                                                                                                                                                                                                                                                                                                     GNKDYHQDVRNNFLPPIIARFIRVNPTQWQQKIAMKMELLGCQFIPKGRPPKLTQPPPPR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTSGCYGTLGMESGVIADPQITASSVLEWTDHTGQENSWKPKKARLKKPGPPWAAFATDE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFMSGIHVSGRGFLASYSVIDKQDLITCLDTASNFLEPEFSKYCPAGCLLPFAEISGTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GERVRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLQMNHSIESKGNEITL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TT-----
                            SFLDSRD-----PASQSQMTSGGDDG 483
                                                          ---MDMSGHPTTSVGQPSTSTFKATGNQPPPLVGTYNTLLSRTDSCSSAQAQYDTPKAGK 739
                                                                                                                       FKP----EE---
                                                                                                                                                                                                                                               ALAAVLVPVLVMVLTTLILILVCAWHWRNRKKKTEGTYDLPY----WDRAGWWKGMKQFL
                                                                                                                                                                                                ---ARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVARKGST 349
                                                                                                                     -GKEAGYADLDPYNSPGQEVYHAYAEPLPITGPEYATPII----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 575.5; DB 4;
Pred. No. 2.4e-40;
4; Mismatches 181;
766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PGM-----
                                                                                                                                                                                                                                                                                                                                        ----NIT-TV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               246
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|-----|----------------------------------------------------------------------|---------|----------------------------------------------------------------------|------------|----------------------------------------------------------------------|--------------|----------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------|---------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------|---------|-----|---------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|------------------------------------------------------------------------------|----------------------|--------------------------------------------------------------------------------------|-----------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------|
| B 8 | ₽                                                                    | QΨ      | В                                                                    | VΩ         | ₽                                                                    | Qy           | g<br>V                                                               | 뮹                                                                    | δĀ                            | PP 94                                                                                                   | B 8                                                                                  | Ma<br>Ma                                                                                                                                                              | QS                                                 |         |     | 무무무                                                                                         |                                                                              | 잡직                                                                           | 22                   | 7 7 X                                                                                | 8 8                                           | 22888                                                                                                                                                     |    | 문무무무                                                                                                                                                                                                  | RESULT<br>Q91ZV2<br>ID Q<br>AC Q                          |
| 251 | 405 GNKDYHKDVRNNFLPPITARFIRVNPVQWQQKIAMKVELLGCQFTLKGRLPKLTQPPPPR 464 | 251 250 | 345 HQWLQIDLNKEKKITGIVTTGSTLIEHNYYVSAYRVLYSDDGQKWTVYREPGAAQDKIFQ 404 | 246 MN 250 | 285 KTSGCYGTLGMESGVIADPQITASSVLEWTDHMGQENSWKPEKARLRKPGPPWAAFATDE 344 | 242 TTPG 245 | 182 DGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLF 241 | 165 LFMSGIHASGRGFLASYSVIDKQDLITCLDTVSNFLEPEFSKYCPAGCLLPFAEISGTIP 224 | LITYASSDHPDLITCLERGSHYFEEKYSK | 68 GKRLITRLGDLNIE-SKTCASDYL-LESSATDQYGPYCG-SWAVPKELRLNSNEVTV 121  : :::   :       :   : ::::::::::::::: | 8 PSYLALLFAVCAPLRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPK 67   :    :    :    : | Query Match 21.2%; Score 565.5; DB 11; Length 769; Best Local Similarity 25.5%; Pred. No. 1.7e-39; Matches 188; Conservative 70; Mismatches 193; Indels 285; Gaps 20; | SEQUENCE 769 AA; 83915 MW; 5B7936C8FA063A93 CRC64; | requiat | , å | EMBL; AF387549; AAL30180.1; - InterPro; IPR000859; CUB_domain. InterPro; IPR000421; FA58.C. | -1- SIMILARITY: BELONGS TO THE CRP/FNR FAMILY OF TRANSCRIPTIONAL REGULATORS. | <pre>yulated after Vascular Injury."; bl. Chem. 276:34105-34114(2001).</pre> | ne Prote<br>al Seque | .4/234;<br>Furukawa Y., Sugai M., Tanigaki K.,<br>A. Sasavama S. Honio T. Tashiro K. | SEQUENCE FROM N.A.:<br>STRAIN=SPRAGUE-DAWLEY; | Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bummalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBL_TaxID=10116; | ** | 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Endothelial and smooth muscle cell-derived neuropilin-like | LT 6<br>V2<br>Q91ZV2 PRELIMINARY; PRT; 769 AA.<br>Q91ZV2; |

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Matches 191
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01-DEC-2001
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PROSITE; PS01180; CUB; 1.
DNA-binding; Transcription regulation.
SEQUENCE 769 AA; 83774 MW; 73C1F16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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J. Biol. Chem. 276:34105-34114(2001).
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Matsumori A., Sasayama S., Honjo T., Tashiro K.;
Matsumori Avel Neuropilin like Membrane Protein Cloned
"ESDN, a Novel Neuropilin like Membrane Protein Cloned
Cells with the Longest Secretory Signal Sequence among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11447234;
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Mammalia; Eutheria;
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                                                              --ATDQYGPYCG-SWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDHPDLITCLE 151
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                                                                                                                                                                                                                                                                                                                                                                                                        191;
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IPR000421; FA58_C.
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Metazoa; Chordata; C
Metazoa; Rodentia; C
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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(TTEMBLIEL. 19, Last sequence update)
(TTEMBLIEL. 21, Last annotation update)
and smooth muscle cell-derived neuropilin-like
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                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 560;
Pred. No. !
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Eukaryotes,
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ryotes, Is
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              Query Match
Best Local :
                             Sugano S., Naganarı A., Sugano S., Naganarı A., Sugano S., Naganarı A., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO55462; BAB70926.1; -
SEQUENCE 155 AA; 16364 MW; 1C150371E07C2217 CRC64;

SEQUENCE 155 AA; 16364 MW; 1C150371E07C2217 CRC64;
                                                                                                                                                                                                                                                            Q96NI2;
Q96NI2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                          Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Is Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T. Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M. Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Sugano S., Nagahari K., Masuho Y., Nagahi K., Isogai T.;
                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         Q96NH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKTEGAYDLPHWDRAGWWKGMKQLLPAKSVDHEETPVRYSTSE--VSHLSAREVT---TV
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              Similarity
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           18.8%;
Score 503; DB
Pred. No. 3.5e
8; Mismatches
                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIALLTGMGIFAIC----RKRK
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           DB 4;
.5e-35;
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                                                                                                                                                      , Inagaki H.,
A., Ishii
                       Length 155;
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                                                                                                            Suzuki
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Matches

103;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Cre
01-NOV-1996 (TrEMBLrel. 01, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Hypothetical 40,0 kDa protein ()
Homo sapiens (Human).
                                                 Q9CX06;
        01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
2400001018Rik protein.
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EMBL; D29810; BAA18909.1; -. INTERPRETED I DENOURS 5 CUB domain.
Interpro; IPR000421; FASE_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "unpublished.";
Submitted (APR-1994) to
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                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004043; LCCL_dom.
Pfam; PF00431; CUB; 1.
Pfam; PF00754; FS_F8_type_C; 1.
SMART; SM00042; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                     YON_TER
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                                                                                                                                                                                                                                                                                          Local
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                                                                                                            HAGVVSNTLGGQISVVISKGIPYYESSLANNVTSVVGHLILQVFFTFKTSG
                                                                                                                         HAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSL-SEKRFLFTTPG
                                                                                                                                                                                                         YLLFSS----ATDQYGPYCG-SWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDH 143
                                                                                                                                                                                                                                      PDLITCLERGSHYFEEKYSKF------CPAGCRDIAGDISGNTKDGYRDTSLLCKAAI
                                                                                                                                                                                              YLRIYNGIGVSRTEIGXYCGLGLQINHSIESKGNEITLLFMSGIHVSGRGFLASYSVIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDSQKPPTHPGTSDSYSAPRDCLTPLNQTAMTALL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PASQSQMT-SGGDDGYSAPRNGLAPLNQTAMTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRVPGPRPTHKHSHSSGGFPPATG-ATQVESYQRPASPKPVGGGYDKPAASSFL--DSRD 469
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ဝ္ဗ
                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                          364 AA;
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                                                                                                                                                                                                                                                                                  Conservative
                                                           PRELIMINARY;
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17,
21,
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                Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                          Score 418; DB 4;
Pred. No. 2.4e-27;
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Catarrhini; Hominidae;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment).
                                                                                                                                                                                                                                                                                                                         FECA6292E9E0801F CRC64;
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; Homo.
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Q8R4W6; Q8R4W6; 01-JUN-2002

(TrEMBLrel. PRELIMINARY;

21,

Created)

PRT;

414

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RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=EMBRYONIC
STRAIN=C57BL/6G; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 2 (EMBL; AK010249; BAB26794.1; MGD; MGI:1923727; Pcolce2.
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                                                                                                                                                                                                                                                                                                                                          142
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InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001
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                                                                                                                                                                                 AVFNGGEVND-----AKRIGKYCGDSPPVPIVSERNELLIQFLSDLSLTADGFIG
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                                                                                                                             RHGSLSEKRFLFTTPGMNITTVAIPSVIFIALLLTGM-GIFAICRKRKKK
                                                                                                                                                                                                                                                                                      RDYPYGYTCVWHIIAPKNQLIELKFEKF-----DVE---RDNY-----CRYDYV
                                                                                                                                                                                                                                                                                                                                          -DHPDLITC----LERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCK----
                                                                               -HYKFRPKKFPTTTTTPVTTTLPV-----
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Pred. No. 1e-06;
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                                                                                                                                                                                                                                  -----LLANGVLS
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; Murinae; Mus
                                                                            302
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Best Local
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Eukaryota; Metazoa; (
Mammalla; Eutheria; )
NCBI_TaxID=10090;
                                                                                                                                                                                                   Q8VBY4;
01-MAR-2002
01-MAR-2002
01-JUN-2002
Strausberg R.;
Submitted (DEC-2001) to the
EMBL; BC022123; AAH22123.1;
EMBL; BC018319; AAH18319.1;
                                            SEQUENCE FROM N.A. TISSUE-LIVER;
                                                                                       Strausberg
                                                                                                  TISSUE-LIVER;
                                                                                                                                            Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                       01-MAR-2002 (TIEMHLIFE! 20, Created)
01-MAR-2002 (TIEMHLIFE! 20, Last sequence update)
01-JUN-2002 (TIEMHLIFE! 21, Last annotation update)
Hypothetical 77.4 kDa protein (Similar to complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steiglitz B.M., Greenspan D.S.;
*Biochemical characterization and expression patterns of t Procollagen COOH-terminal proteinase enhancer protein 2.*;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF352788; AAL83947.1; -.
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01-JUN-2002
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                              subcomponent)
                                                                                                                                                                                                                                                 Q8VBY4
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                                                                             (JAN-2002)
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Metazoa; Chordata; C
---+heria; Rodentia; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 AA;
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                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                    (Mouse).
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Rodentia;
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Last annotation update)
roteinase enhancer prote
                      EMBL/GenBank/DDBJ
                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 178;
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                                                                                                                                            Craniata; Veri
Sciurognathi;
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                                                                                                                                              Muridae;
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                       databases.
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                                                                                                                                             Murinae;
                                                                                                                                                                                        component
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                                                                                                                                              Mus
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Best Local :
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InterPro; IPR000436; Sushi_SCR_
Pfam; PF00431; CUB; 2.
Pfam; PF00008; EGF; 1.
Pfam; PF00084; sushi; 2.
Pfam; PF00084; sushi; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                      09UKZ9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Procollagen C-terminal proteinase enhancer protein
          Kumar
Sathe
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-20334622; PubMed-10873381;
MEDLINE-20334622; PubMed-10873381;
Xu H., Acott T.S., Wirtz M.K.;
"Identification and Expression of
Proteinase Enhancer Protein Gene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                       SEQUENCE FROM N.A.
TISSUE-OSTEOARTHRITIC CARTILAGE;
MEDLINE-21482651; PubMed-11597177;
Kumar S., Connor J.R., Dodds R.A.,
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00010; ASX_HYDROXYL; UNKN
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF_CA; UNKNOWN_1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNO
                                                                                                                               Genomics
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InterPro;
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InterPro;
InterPro;
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SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 FCSCPPEYFLHDDMRNCGVNCSGDVFTALIGEISSPNYPNPYPENSRCEYQIQLQEGFQV
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          လ လ
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SM00020;
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                                                                                                                             66:264-273(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000859;
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IPR001314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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; Tryp_SPc; 1.
10; ASX_HYDROXYL;
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                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
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Sushi_SCR_CCP.
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P .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
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Pred. No. 7.1e-06;
                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   ne from
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          Badger
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      Halsey W.
dger A.M.,
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om the
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Glaucoma Candidate
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      en M.,
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Best Local
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 SEQUENCE FROM N.A. MEDLINE-98192519; p Sakai H., Nakashima Nozawa Y.;
                                                                                                                                                              070542
070542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; F
PROSITE; F
Collagen.
SEQUENCE
                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequenced tags (ESTs) each from adult huma cartilage cDNA libraries.", Osteoarthritis Cartilage 9:641-653(2001).
-i- SIMILARITY: CONTAINS 2 CUB DOMAINS.
EMBL; AF098269; AAF04621.1; -.
EMBL; AY035400; AAK63128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00042; CUB; 2
PROSITE; PS00211; ABC_:
PROSITE; PS01180; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00431; CUB; 2. Pfam; PF01759; NTR; 1.
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InterPro; IPR000859; CUB_domain.
                                                                                                  Rattus norvegicus (Rat).
                                                                                                             Serine protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lark M.W.;
"Identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRLNSNEVTVLFKSGSHISGRGFLLTYASS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KITVPEGKVVVLNFRFIDLESDNLCRYDFV-----DVYNGHANGQRIGRFCGTFR-PGA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGPSVLALLFAVCAPLRLQ--AEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEK 61
                                                                                                                                                                                                                                                                                      TVSIINIYKEGNLAIQQAGKNMSARLTVVCK---
                                                                                                                                                                                                                                                                                                                                                          SVIFIALLLTGM-GIFAICRKRKK-----GNPYVSADAQKTGCWKQIKYPFARHQSTEF
                                                                                                                                                                                                                                                                                                                                                                                   PPAPIVSER-----NELLIQFLSDL-SLTADGFIGHY--IFRPKKLPTTTEQPVTT-TFP
                                                                                                                                                                                                                                                                                                                                    -----VTTGLKPTVALCQQKCRRTGTLEGN-YCSSDFVLAG---TVITTITRDGSLHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IITVPKGKRLILRLGDLNIES-KTCASDYLLFSSATDQY------GPYCGSWAVPKE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTG-ESGFIGSEGFPGVYPPNSKCTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99; Conser
               Nakashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 AA;
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                         PubMed=9524231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                            ----EKEMTQKLDLITSDMADYQQPLMIGTGTVARKGSTFRPMDTD
           s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45716 MW;
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              Yoshimura
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Last annotation updat
                                                                                                                                                  Created)
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Pred. No. 4.5e
57; Mismatches
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from adult human n
                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B9AA87FD9AAF7A5B CRC64;
           s;
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            Nishimura
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                                                                                                                                                                                                                                                                                      -QCPLL---
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                                                                                                                         update)
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            Y.,
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and osteoarthritic
                                                                                     Euteleostomi;
            Sakai
                                                                          Murinae;
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Best Local S
Matches 52
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Pfam; PF00089; trypsin; 1.
PRINTS; PF00072; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00019; EGF CA; 1.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000561; E
InterPro; IPR001284; E
InterPro; IPR001254; S
InterPro; IPR000436; S
Pfam; PF000431; CUB; 2.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01240; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Calcium-binding; EGF-1ike domain; Glycoprotein; Hydrolase; Protease; Repeat; Serine protease.

SEQUENCE 694 AA; 77788 Mm. CTCC---
                                                                                                                 O8R099 PRELIMINARY; PRT; 694 AA. 08R099; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 51milar to complement component 1, s subcomponent.
 Strausberg R.;
Submitted (APR
                        SEQUENCE FROM N.A.
TISSUE-SALIVARY GLAND;
                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D88250;
HSSP; P00763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          during glial differentiation.";
Gene 209:87-94(1998).
-!- SIMILARITY: CONTAINS 2 CUB
                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000152;
InterPro; IPR001314;
InterPro; IPR000859;
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                                                                                                                                                                                                                                                      NV-GST
                                                                                                                                                                                                                                                                                                           DLTGQNKGWKLRY---
                                                                                                                                                                                                                                                                                                                                                           VLTIRREDFDVEPADSEGNCHDSLTFAAKNQQFGPYCGNGFPGPLTIKTQSNTLDIVFQT
                                                                                                                                                                                                                                                                                                                                                                                                                FCSCPPEYFLHDDMRTCGVNCSGDVFTALIGEIASPNYPNPYPENSRCEYQIRLQEGFRL
                                                                                                                                                                                                                                                                                                                                GSHISGRGFLLTYASSDHPDLITC------LERGSHYFEEKYSKFCPAGCRDIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                        FAVCAP---LRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRL
                                                                                                                                                                                                                                                                                                                                                                                     IL--RIGDINIE----SKTCASDYLLFSSATDQYGPYCGS-WAVPKELRINSNEVTVLFKS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 6.3%; Score 169.5; Similarity 28.0%; Pred. No. 1.2 52; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S01.193;
(APR-2002)
                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ser_protease_Try.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                           HGDPIPCPKEISANSIWEPEKAKYVFKDVVKITCVDGFEVVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CUB DOMAINS
                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2e-05;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a serine protease homologous to glial cells and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                             Murinae;
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                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC027183; AAH27183.1; -. SEQUENCE 694 AA; 77713 MW; 455A9EE10C8CC12F CRC64;
                                                           337 NV-GST 341
                                                                              175 DISGNT 180
                                                                                                                                                                               281 DLTGQNKGWKLRY----HGDPTPCPKEISANSIWEPEKAKYVFKDVVKITCVDGFEVVEG 336
                                                                                                                                                   126 GSHISGRGFLLTYASSDHPDLITC------LERGSHYFEEKYSKFCPAGCRDIAG 174
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1: /cgn2_6/ptodata/1,
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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6: /cgn2_6/ptodata/1,
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2671
1 MGTGAGGPSVLALL
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Gapop 10.0 , Gapext 0.5
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US-08-866-650-3
US-09-021-087-3
US-09-021-087-3
US-09-021-08-93-008-9
US-08-939-008-9
US-08-939-08-93-08-93-08-93-08-93-08-93-08-93-08-93-135-18
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| 45                | 44              | 43              | 42               | 41              | 40              | 39               | 38              | 37              | 36               | 35              | 34                | S<br>S          | 32                | 31                | 30                | 29                | 28                |
|-------------------|-----------------|-----------------|------------------|-----------------|-----------------|------------------|-----------------|-----------------|------------------|-----------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| 116               | 116.5           | 118             | 119              | 121             | 121             | 121              | 121             | 121             | 121              | 125.5           | 125.5             | 125.5           | 126               | 126.5             | 126.5             | 129.5             | 129.5             |
| 4.3               | 4.4             | 4.4             | 4.5              | 4.5             | 4.5             | 5                | .5              | 4.5             | <b>.</b> 5       | 4.7             | 4.7               | 4.7             | 4.7               | 4.7               | 4.7               | 4.8               | 4.8               |
| 1180              | 730             | 102             | 902              | 1083            | 1083            | 1083             | 1019            | 1019            | 1019             | 1785            | 666               | 468             | 401               | 855               | 855               | 931               | 926               |
| 4                 | 4               | 4               | 4                | N               | N               | H                | N               | N               | H                | 4               | 4                 | N               | N                 | 4                 | N                 | w                 | ω                 |
| US-09-206-942-65  | US-08-872-757-2 | US-09-374-135-7 | US-09-644-600-10 | US-08-877-620-2 | US-08-596-405-2 | US-08-296-014A-2 | US-08-877-620-4 | US-08-596-405-4 | US-08-296-014A-4 | US-09-341-587-3 | US-09-341-587-1   | US-08-839-008-7 | US-08-839-008-5   | US-09-644-600-2   | US-09-027-337-2   | US-08-936-135-16  | US-08-936-135-14  |
| Sequence 65, Appl | N               | 7,              | ,01              | Ņ               | 2               | ν,               | 4,              | .4              | 4                | ω               | Sequence 1, Appli | 7,              | Sequence 5, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 16, Appl | Sequence 14, Appl |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08936135 Patent No. 6054293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
            TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Tessie
                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UNMBER: 36,627
REFERENCE/DOCKET NUMBER: UC:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, Har
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: He, Zhigang
   LENGTH:
                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                           TELEPHONE:
                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSIINIYKEGNLAIQQAGKNMSARLTVVCK-----QCPLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISYDN------EKEMTQKLDLITSDMADYQQPLMIGTGTVARKGSTFRPMDTD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPAPIVSER----NELLIQFLSDL-SLTADGFIGHY--IFRPKKLPTTTEQPVTT-TFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IITVPKGKRLILRLGDLNIES-KTCASDYLLFSSATDQY------GPYCGSWAVPKE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTG-ESGFIGSEGFPGVYPPNSKCTW 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VTTGLKPTVALCQQKCRRTGTLEGN-YCSSDFVLAG---TVITTITRDGSLHA
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                                                                                                                                                                                                                                                                                                  94010
923 amino acids
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23.1%; Pred. No. 1.8e-08;
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RESULT 3
US-08-872-757-4
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; MOLECULE TYPE:
US-08-936-135-6
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Best Local Similarity 19.3
Matches 104; Conservative
                                                                                                              574 LGLRMELLGCEVEAPTAGPTTPNGNPVHECDDDQANCHSGTGDDF-QLTGGTTVLATEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 ---ANGVLSRHGSLSEKRFLFTTPGMNITTVAIPSVIF----IALLLTG-------MGI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 IRYEIFKRGPECSQNYTA-PTGVIKSPGFPEKYPNCLECTYIIFAPKMSEIILEFESFDL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 LRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDLNI 80
                                                                                                                                                                                                                                                                                                                                        DRNWMPENIRLVTSRTGWALPPSPHPYTNEWLQVDLGDEKIVRGVIIQGGKHRENKVFMR
                                                                                                                                                                 --VERHLLRAHTFSTQSGYRVPGPRPTHK------HSHSSGGFPPATGATQVESYQRP 446
                                                                                                                                                                                                                      KFKIAYSNNGSDWKTIMDDSKRKAKSFEGNNNYDTPELRTFSPLSTRFIRIYPERATHSG
                                                                                                                                                                                                                                                                               ----TVARKGSTFRPMDTDTEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPEYATPI- 396
                                                                                                                                                                                                                                                                                                                                                                                                    EKE-MTQKLDLITS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSKPLITRFVRIKPVSWETGISMRFEVYGC-KITDYPCSGMLGMVSGLISDSQITASNQA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FA-----ICRKRKKGNPYVSADAQKTGCWKQIKYPFARH-----QSTEFTISYDN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVGTQGAISKE----TKKKYYVKTYRVDISSNGEDWISLKEGNKAIIFQGNTNPTDVVLGV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IHSDQITASSQYGTNWSVERSRLNYPENGWTPGEDSYKEWIQVDLGLLRFVT 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQDSNPPGGMFCRYDRLEIWDGFPEVGPHIGRYCGQ-KTPGRIRSSSGVLSMVFYTDSAI
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19.3%;
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Sequence 4, Applia Patent No. 625858 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: APPLICANT: APPLICANT: APPLICANT: APPLICANT: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: U.S.A. ZIP: 10036-2711 CITY: New York STATE: New York ADDRESSEE: INFORMATION: Application US/08872757 1155 Avenue of the Americas Sieron, Aleksander Prockop, Darwin Hojima, Yoshio Li, Shi-Wu Pennie & Edmonds Floppy disk PROCESSES; METHODS AND USES THEREOF RECOMBINANT C-PROTEINASE AND Darwin J. US/08/872,757

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                                                                                                                                                                                                                                                                                                                                                                      SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                          TITLE OF INVENTION: RECOMP
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REFERENCE/DOCKET NUMBER: 831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
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                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                               COUNTRY:
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TOPOLOGY: linear
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APPLICATION NUMBER:
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E: New York
RY: U.S.A.
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             APPLICATION DATA:
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                                                                                                                                                                                1155 Avenue of the Americas
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                             PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                               Prockop,
                                                                                                                                                                                                                                                                                                                     Li, Shi-Wu
                                                                                                                                                                                                 Pennie & Edmonds
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US/08/572,225
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Pred. No. 1.8e-05;
37; Mismatches 75;
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US-08-866-650-3
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Best Local Similarity 33.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                               TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                              LENGTH: 1013 amino acids
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 53703
                                  TOPOLOGY:
                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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STRANDEDNESS: unl
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                                                                                                                             TELEPHONE:
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                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
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                            99 ---YGPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYAS----- 140
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                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                         NAME: Berson, Bennett
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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SPILGRLCGS-KIPDPLMATGNEMFIRFISDASVQRKGFQATHSTECGGRLKAESKPRDL 900
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                                                                                                                                                                                                                                                                                              608-251-9166
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26.5%;
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Pred. No. 3.9e-05;
                                                                                                                      Score 139; DB Pred. No. 3.9e
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US-09-240-473-3
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                                                                                                                            RESULT 8
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                                                                   Patent No. 5916758
GENERAL INFORMATION:
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Best Local S
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APPLICANT: Takahara,
APPLICANT: Hoffman,
                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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TELEPHONE: 608-251-5000
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CORRESPONDENCE ADDRESS:
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McDonnell, Peter (
McNulty, Dean E
Rosen, Craig A
Siemens, Ivo R
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                                                         Hurle, Mark R
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SYSTEM: PC-DOS/MS-DOS
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26.5%;
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Pred. No. 3.9e-05;
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                                                                             Patent No. 5916758
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                                                               GENERAL INFORMATION:
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                  APPLICANT:
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NAME: Baumeister Kirk
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NUMBER OF SEQUENCES:
   APPLICANT:
                   APPLICANT:
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Yue, Tian-Li
McDonnell, Peter C
McNulty, Dean E
Rosen, Craig A
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                                             Hurle, Mark R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33,833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 137; DB 2;
Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                   EKYSKFCPAGCR-DIAGDISGNTKDGYRDTSLLCK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98;
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                                    US-08-991-408-4
                                                   RESULT 10
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Sequence 4, Appl. Patent No. 60080
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yue, Tiar TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                   181
                                                                                                   238 DAVPGSISSE 247
                                                                                                                                    193 AAIHAGIITD 202
                                                                                                                                                                                                                                121 VAPGNQVTLRMTTDEGTGGRGFLLWYSGRATSGTEHQFCGGRLEKAQGTLTTPNWPESDY 180
                                                                                                                                                                                                   144 PDLITCLERGSHYFE---
                                                                                                                                                                                                                                                                                                 63 CIWTITVPEGQTVSLSFRVFDLELH-PACRYDALEVFAGSGTSGQRLGRFCGTFR-PAPL 120
                                                                                                                                                                                                                                                                                                                                    59
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   4 AATASLLGPLLTACALLPFAQGQTPNYTRPVFLCGGDVKG-ESGYVASEGFPNLYPPNKE: 62
                                                                                                                                                                                                                                                                                                                                                                                                5 AGGPSVLALLFAVCAPLRLQAEELGDG-----CGHIVTSQDSGTMTSKNYPGTYPNYTV 58
                                                                                                                                                                                                                                                                                                                                CEKIITVPKGKRLIL--RLGDLNIESKTCASDYL-LFS---SATDQYGPYCGSWAVPKEL 112
                                                                                                                                                                 PPGISC---SWHIIAPPDQVIALTFEKFDLEPDTYCRYDSVSVFNGAVSDDSRRLGKFCG
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Young, Peter R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                  US/08991408
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Pred. No. 2.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 449;
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GENERAL INFORMATION:

APPLICANT:

ARLETH, ANTHONY J. WILLETTE, ROBERT N

ELSHOURBAGY, NABIL A

APPLICANT:

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                                                                                                                            GENERAL INFORMATION:
                                                                                                                                          Sequence 4, Application US/09432473 Patent No. 6365715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN FILE REFERENCE: ATG-50038-D1
CURRENT APPLICATION NUMBER: US/09/432,473
                                                                   APPLICANT: ARLETH, ANTHONY J. APPLICANT: WILLETTE, ROBERT N. APPLICANT: ELSHOURBAGY, NABIL A.
                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: 60/
FILING DATE: 02-JAN-199
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MEDIUM TYPE: Diskett
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                      335
                                                                                                                                                                                                                                                                                                                         293 DNTVSKKGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 CEP----GYELGPDRRSCEAACGGLLTKL-NGTITTPGWPKEYPPNKNCVWQVVAPTQYR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 CAPLRIQAEEIGD------GCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKR 70
                                                                                                                                                                                                                                                                                                                                                                                                                            71 LILREGDENIE-SKTCASDYLL----FSSATDQYGPYCGSWAVPKELRENSNEVTVLFKS 125
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TOPOLOGY: 111
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                                                                                                                                                                                                                                                                                   KDGY--RDTSLLCKAA----IH--AGIIT 201
                                                                                                                                                                                                                                                    RNGFVLHDNKHDCKEAECEQKIHSPSGLIT 364
                                                                                                                                                                                                                                                                                                                                                      GSHISGRGFLLTYASSDHPDLITCLERGSHYFEEK--YSK---FCPAGCRDIAGDISGNT
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for Windows Version
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Pred. No. 4.1e-05;
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                                                                                                                                                                                                                                                                                                                      --KAHFFSDKDECSKDNGGCQHECVNTMGSYMCQC 334
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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EARLIER APPLICATION NUMBER: 08/991,408
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 60/034,471
EARLIER FILING DATE: 1997-01-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ
                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 591
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                 LENGTH: 1013 amino acids
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                                                                                                                                                                            NAME: Berson, Bennett
REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 LILRLGDLNIE-SKTCASDYLL----FSSATDQYGPYCGSWAVPKELRLNSNEVTVLFKS 125
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                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 53703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                        FILING DATE:
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                 POPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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TYPE:
                                amino acid
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                                                                                                        608-251-9166
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                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
               linear
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                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian Tolloid-Like Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kazuhiko
                                                                                                                                                                                                                                                                       US/08/866,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daniel S
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US-09-021-287-5
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                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Appli
Patent No. 598171
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                                                  Matches
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INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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APPLICATION NUMBER:
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32 CGHIVTSQDSGTMTSKNYPGTYPNYTYCEKIITVPKGKRLILRLGDLNI-ESKTCASDYL 90
                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                   NAME: Berson, Bennett
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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1 South Pinckney Street
                                                                                                                                                                          1013 amino acids
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                                                                                                                         protein
                                                              5.1%;
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                                               31;
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Pred. No. 0.0001;
                                                              Score 135; DB 2;
Pred. No. 0.0001;
                                               Mismatches
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                                            67; Indels 42;
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                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                  349 CGETL-QESNGNLSSPGFPNGYPSYTHCIWRVSVTPGEKIVLNFTTMDLYKSSLCWYDYI 407
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91 LFSSATDQY------GPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDH 143
                                                                            32 CGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDLNI-ESKTCASDYL 90
                                                                                                                             Local Similarity
                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                Conservative
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                                                                                                                             Score 135; DB 3; Pred. No. 0.0001;
                                                                                                              Mismatches
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                                                                                                                                          Length 1013;
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US-09-240-473-5
                                                                                                                                                                                                                                                                                          Query Match 5.1%;
Best Local Similarity 23.1%;
Matches 42; Conservative 3
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino aci
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|:
501 GL 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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501 GL 502
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APPLICANT: Hoffman
TITLE OF INVENTION:
                                    198 GI 199
                                                                                                        144 PDLITCLERGSHYFEEKYSKFCPAGCRDIAGDI-SGNTKDGYRDT-----SLLCKAAIHA 197
                                                                          461
                                                                                                                                                                                                                     349 CGETL-QESNGNLSSPGFPNGYPSYTHCIWRVSYTPGEKIVLNFTTMDLYKSSLCWYDYI 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 PDLITCLERGSHYFEEKYSKFCPAGCRDIAGDI-SGNTKDGYRDT-----SLLCKAAIHA 197
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                                                                                                                                                                      91 LFSSATDQY------GPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDH 143
                                                                                                                                                                                                                                              32 CGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLILRLGDLNI-ESKTCASDYL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/240,473
                                                                                                                                               ---EVRDGYWRKSPLLGRFCGD-KLPEVLTSTDSRMWIEFRSSSNWVGKGFAAVYEA--- 460
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VENTION: Mamumalian Tolloid-Like Protein
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31; Mismatches 67; Indels 4
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Search completed: May 15, 2003, 13:15:23 Job time : 16.5632 secs

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                                       US-09-823-038A-51
US-10-003-132-6
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US-09-759-130B-78
US-09-759-130B-78
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Sequence 6, Appli
Sequence 7, Appli
Sequence 75, Appl
Sequence 75, Appl
Sequence 76, Appl
Sequence 78, Appli
Sequence 3, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 104, App
                                                                                                                                                                                                                                                                                                                   Description
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Sequence 51, App
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| Query<br>Best<br>Match                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence - Publicati General II APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN II I CURRENT I CURRENT I CURRENT I CURRENT I CURRENT I NUMBER OI SOFTWARE FILE RICH APPLICATION OF APPLICAN APPLICA | 44444000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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| similarity ; Conservati ; Conse | plication . USZ00201 ATION: XX. Brian A shoemaker. NWTION: NEU CATION NEU GATION NUMBE TATE: 2000 DATE: 2000 DATE: 2000 DATE: 2000 STRING NUMBE TESEO for W                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 100.0%; servative 0; lity 100.0%; servative 0; o; all lilling little lit | on US/1<br>2019279<br>2019279<br>1 A.<br>1 A.<br>1 C. Kimk<br>VEUROPP<br>VWHER: U<br>2001<br>2001<br>2001<br>109<br>119<br>109<br>119<br>109<br>119                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 415<br>415<br>415<br>415<br>415<br>415<br>415<br>415<br>415<br>415                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| tch 100.0%; Score 2671; DB 9; Length 503; al Similarity 100.0%; Pred. No. 4.3e-210; S03; Conservative 0; Mismatches 0; Indels 0; GMGTGAGGFSVLALLFAVCAPELLADAEELGDGCGHIVTSQDSGTWTSKNYPGTYPNYTVCE MGTGAGGPSVLALLFAVCAPLRIQAEELGDGCGHIVTSQDSGTWTSKNYPGTYPNYTVCE MGTGAGGPSVLALLFAVCAPLRIQAEELGDGCGHIVTSQDSGTWTSKNYPGTYPNYTVCE KIITVPKGKRLILRLGDLNIESKTCASDYLLFSSATDQYGPYCGSWAVPKELRLNSNEVT KIITVPKGKRLILRLGDLNIESKTCASDYLLFSSATDQYGPYCGSWAVPKELRLNSNEVT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 3/10003132<br>2750A1<br>E. IDSTILIN HOMOLOG ZCUB5<br>21-11-15<br>21-11-15<br>21-11-15<br>21-15<br>31-11-15<br>31-11-15<br>31-11-15<br>31-11-15                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | US-09-906-838-104 US-09-907-613-104 US-09-904-820-104 US-09-904-820-104 US-09-904-859-104 US-09-904-786-104 US-09-906-700-104 US-09-903-749a-1104 US-09-903-736-104 US-09-903-736-104 US-09-903-736-104 US-09-904-119-1104 US-09-904-119-1104 US-09-904-119-1104 US-09-904-119-1104 US-09-904-119-1104 US-09-904-119-1104 US-09-904-119-1104 US-09-904-119-1104 US-09-904-553-104 US-09-905-056-104 US-09-905-381-104 US-09-905-381-104 US-09-905-381-104 US-09-905-381-104 US-09-905-381-104 US-09-905-088-104 US-09-905-088-104 |
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 503
TYPE: PRT
ORGANISM: Mouse
US-09-823-038A-51
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APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 1100.1037c3
CURRENT FAPELICATION NUMBER: US/09/823,038A
CURRENT FILLING DATE: 2001-07-09
 301
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ARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVARKGSTFRPMDTDTEEV
                                                   FTTPGMNITTVAIPSVIFIALLLTGMGIFAICRKRKKKGNPYVSADAQKTGCWKQIKYPF
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Pred. No. 4.1e-209;
1; Mismatches 1;
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US-10-003-132-6
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PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 19
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APPLICANT: GAO, ZETEN
APPLICANT: Shoemaker, Kimberly E.
TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCU
TILE REFERENCE: 00-62
CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows
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nes 458; Conserv
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                             ARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVARKGSTFRPMDTDTEEV
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DDGYSAPRNGLAPLNQTAMTALL
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ilarity 91.1%;
Conservative
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Pred. No. 1.2e-187;
0; Mismatches 0;
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LENGTH: 715
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CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILLING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/249,004
PRIOR FILLING DATE: 2000-11-15
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APPLICANT: Gao, Zeren
APPLICANT: Shoemaker, Kimberly E.

TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCUB5
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SOFTWARE: FastSEQ for Windows Version 3.0
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KGSTFRPMDTDTEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPEYATPIVERHLLRAH
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                                                        KGSTFRPMDTDAEEAGVSTDAGGHYDCPQRAGRHEYALPLAPPEPEYATPIVERHVLRAH
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US-09-759-130B-73
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CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
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Best Local :
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
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TITLE OF INVENTION: MOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-09-10
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185 RDTSLLCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRELF---
                                                                                                                                                                                              14 AAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTIT
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                                                              SGSHISGRGFLLTYASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGY 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Kirst, Susan J
Mackay, Charles R
Myers, Paul S
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Sharp, John I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCarthy, Seam of the Seam of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leiby, Kevin R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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2 for Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.1%; 55.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1924.5;
Pred. No. 7.3e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3e-149;
hes 73;
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RESULT 6
US-09-759-130B-75
                                          CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR APPLICATION NUMBER: US 09/596,364
PRIOR APPLICATION NUMBER: US 09/342,364
                                                                                                                                                                                                                                                                                                                                APPLICANT: Millennium Pharmaceuticals, In
APPLICANT: McCarthy, Sean A
APPLICANT: McCarthy, Sean A
APPLICANT: Sharp, John D
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Leiby, Kevin R
APPLICANT: Leiby, Kevin R
APPLICANT: Witghton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Goodearl, Andrew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 75, Application US/097591308 Publication No. US20030022279A1
                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL GENES
TITLE OF INVENTION: PROGNOSTIC
TITLE OF INVENTION: USES.
FILE REFERENCE: MPIO0-5350MNIM
                                                                                                                                                                                                                                                                                                                       APPLICANT:
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   FILING DATE: 1999-06-29
APPLICATION NUMBER: US 09/608,452
FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                     I: Holtzman, Douglas A INVENTION: NOVEL GENES INVENTION: PROGNOSTIC,
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US-09-759-130B-76; Sequence 76, Application US/09759130B; Publication No. US20030022279A1; GENERAL INFORMATION: APPLICANT: Millennium Pharmaceutical:
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; ORGANISM: Homo
US-09-759-130B-75
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SEQ ID NO 75
LENGTH: 681
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                                                                                                                           GYSAPRNGLAPLNQTAMTALL
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377; Conserv
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 Pharmaceuticals,
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PRIOR APPLICATION NUMBER: US 09/420,707 PRIOR FILING DATE: 1999-10-19 NUMBER OF SEQ ID NOS: 460
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PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                      361 VPQTWHQRIALKVELIGCQITQGNDSLVWRKTSQSTSVSTKKEDETITRPIPSEETSTGI 420
                                                                           LITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDELG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSGGFPPATG-ATQVESYQRPASPKPVGGGYDKPAASSFL--DSRDPASQSQMT-SGGDD 482
                                                                                                                                                                                  EFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVARKGSTFRPMDTDTEEVRVNTEA
                                                                                                                                                                                                                                             NITTVAIPLVLLVVLVFAGMGIFAAFRKKKKKGSPYGSAEAQKTDCWKQIKYPFARHQSA
                                                                                                                                                                                                                                                               NITTVAIPSVIFIALLLIGMGIFAICRKRKKKGNPYVSADAQKTGCWKQIKYPFARHQST 306
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SSGGFSPVAGVGAQDGDYQRPHSAQPADRGYDRPKAVSALATESGHPDSQKPPTHPGTSD
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                                                                                                                                                             EFTISYDNEKEMTQKLDLITSDMADYQQPLMIGTGTVTRKGSTFRPMDTDAEEAGVSTDA
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Pred. No. 1.4e
33; Mismatches
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RESULT 8
US-09-759-130B-78
; Sequence 78, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
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Best Local s
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NUMBER OF SEQ ID NOS:
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APPLICANT:
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PRIOR FILING DATE: 2000-01-07
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PITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
PITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
PITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILE REFERENCE: MPI00-5350MNIM
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LENGTH: 421
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FILING DATE: 2000-04-27
APPLICATION NUMBER: US 09/578,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/602,871 FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/393,996 FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-06-29
APPLICATION NUMBER: US 09/608,452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-05-24
APPLICATION NUMBER: US 09/333,159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/420,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/342,364
                                                                                                                                                                                                                                                                                                                  LITCLERASHYLKTEYSKFCPAGCRDVAGDISGNMVDGYRDTSLLCKAAIHAGIIADELG
                                                                                                                                                                                                        LITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTKDGYRDTSLLCKAAIHAGIITDELG
                                                                                                                                                                                                                                                     ASDYLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYASSDHPD
                                                                                                                             GQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLFTSNG
                                                                                                                                                                                                                                                                       ASDYLLFSSATDQYGPYCGSWAVPKELRLNSNEVTVLFKSGSHISGRGFLLTYASSDHPD 145
Millennium Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCarthy, Seam ..
Frager, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wrighton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mackay, Charles R
Myers, Paul S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kirst, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leiby, Kevin R
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1999-10-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrew
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                                                                                                                                                                                                                                                                                                                                                                                                  37.3%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                Score 995; DB 9; L
Pred. No. 3.3e-73;
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                                                                                                                                                         245
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                  0,
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US-10-060-830-3

Sequence 3, Application US/10060830
Publication No. US:20030032154A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: HUMAN LCCL DOM

DOMAN

CONTAINING

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; ORGANISM: Homo
US-09-759-130B-78
RESULT
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PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Matches
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FILE REFERENCE: MPIO0-5350MNIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                            452 VGGGYDKPAASSFL--DSRDPASQSQMT-SGGDDGYSAPRNGLAPLNQTAMTALL 503
                                                                                                                               121
                                                                                                                                               393 ATPIVERHLLRAHTFSTQSGYRVPGPRPTHKHSHSSGGFPPATG-ATQVESYQRPASPKP
                                                                                                                                                                                                                         333 QQPLMIGTGTVARKGSTFRPMDTDTEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPEY
                                                                                                                                                                                                                                                                                                273 RKRKKKGNPYVSADAQKTGCWKQIKYPFARHQSTEFTISYDNEKEMTQKLDLITSDMADY 332
                                                    181
                                                                                                                                                                                                    61 QQPLMIGTGTVTRKGSTFRPMDTDAEEAGVSTDAGGHYDCPQRAGRHEYALPLAPPEPEY
                                                                                                                                                                                                                                                                            1 RKKKKKGSPYGSAEAQKTDCWKQIKYPFARHQSAEFTISYDNEKEMTQKLDLITSDMADY 60
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                                                    ADRGYDRPKAVSALATESGHPDSQKPPTHPGTSDSYSAPRDCLTPLNQTAMTALL
                                                                                                                           ATPIVERHVLRAHTFSAQSGYRVPGPQPGHKHSLSSGGFSPVAGVGAQDGDYQRPHSAQP
                                                                                                                                                                                                                                                                                                                                                         176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATION NUMBER: US 09/393,996
DATE: 1999-09-10
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Susan J
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                                                                                                                                                                                                                                                                                                                                                                        33.48;
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                                                                                                                                                                                                                                                                                                                                                                        Score 893; DB 9;
Pred. No. 3.2e-65;
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                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Length 235;
                                                                                                                                                                                                                                                                                                                                                       Indels
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PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR APPLICATION NUMBER: US 60/325,062
PRIOR APPLICATION NUMBER: US 60/325,062
PRIOR FILLING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 1123
SOFFWARE: Acomica Sequence Listing Engine
SEQ ID NO 3
LENGTH: 729
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-830-3
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR TELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.5%; Score 575.5; DB 9; Length 729; Best Local Similarity 24.5%; Pred. No. 1.4e-38; Matches 183; Conservative 84; Mismatches 181; Indels 299;
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CURRENT APPLICATION NUMBER: US/10/060,830
CURRENT FILING DATE: 2002-01-30
350 FRPMDTDTEEVRVNTEASGH-----YDCPHRPGRHEYALPLTHSEPEYATPIVERHLLRA 404
                                                                   302 YQWLQIDLNKEKKITGIITTGSTMVEHNYYVSAYRILYSDDGQKWTVYREPGVEQDKIFQ 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 KTSGCYGTLGMESGVIADPQITASSVLEWIDHTGQENSWKPKKARLKKPGPPWAAFAIDE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 DGYRDTSLLCKAAIHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLF 241
                                                                                                                                                                                                                                                                                                                                                        362 GNKDYHQDVRNNFLPPIIARFIRVNPTQWQQKIAMKMELLGCQFIPKGRPPKLTQPPPPR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 LFKSGSHISGRGFLLTYASSDHPDLITCLERGSHYFEEKYSKFCPAGCRDIAGDISGNTK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                AIPSVI--FIALLIGMGIFAIC-----RKRKKKGN---PYVSADAQKTGCWKQIKYPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFMSGIHVSGRGFLASYSVIDKQDLITCLDTASNFLEDEFSKYCPAGCLLPFAEISGTIP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERVRIKFGDFDIEDSDSCHFNYLRIYNGIGVSRTEIGKYCGLGLOMNHSIESKGNEITL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKRLILRLGDLNIE-SKTCASDYLLFSS----ATDQYGPYCG-SWAVPKELRLNSNEVTV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLFLLLLVLLLLEDAGAQQGDCCGHTVLGPESGTLTSINYPQTYPNSTVCEWEIRVKM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSVLALLFAVCAPLRLQAEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPK 67
                                                                                                                                                                                                                                                                 NSNDLKNTTAPPKIAKGRAPKFTQPLQPRSSNEFPAQTEQTTASPDIRNTTVTPNVTKDV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PGM----- 246
                                                                                                                                                                                                                                                                                           ----NIT-TV 251
                                                                                                                                                                                                                                                                                                                                                                                                         ----- 246
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|     | PPRNSNDLKNTTAPPKIAKGRAPKFTQPLQ 372                            | 313 QWQQKIAMKMELLGCQFIPKGRPPKLTQPP                                     | 문        |
|-----|---------------------------------------------------------------|------------------------------------------------------------------------|----------|
|     | 246                                                           | y 247                                                                  | Qy       |
|     | IFQGNKDYHQDVRNNFLPPIIARFIRVNPT 312                            | b 253 NYYVSAYRILYSDDGQKWTVYREPGVEQDKIFQGNKDYHQDVRNNFLPP                | В        |
| •   | 246                                                           | y 244                                                                  | γo       |
|     | DEYQWLQIDLNKEKKITGIITTGSTMVEH 252                             | b 193 EWTDHTGQENSWKPKKARLKKPGPPWAAFATDEYQWLQIDLNKEKKITGIITTGSTMVEH     | 망        |
|     | 243                                                           | y 244                                                                  | ν        |
|     | *LETT 243<br>                                                 | y 209 NLLQSKGISHEGLLANGVLSKHGSLSEKRFLETT                               | ρ d<br>2 |
|     |                                                               | . 73                                                                   | , B 7    |
|     |                                                               | 148<br>148                                                             | \$ B 5   |
| 18; | aps 1                                                         | Ca                                                                     |          |
|     |                                                               | TYPE: PI<br>ORGANISM                                                   | US ;     |
|     | Engine                                                        | ARE: Aeomica Sequence Listing NO 1114                                  |          |
|     | 52                                                            | LICATION  <br>ING DATE:<br>SEQ ID N                                    |          |
|     | 51                                                            | APPLICATION NUMBER: US 09/864,7 FILING DATE: 2001-05-23                |          |
|     | 563                                                           | APPLICATION NUMBER: PCT/US01/00 FILING DATE: 2001-01-30                | ···      |
|     | 568 .                                                         | APPLICATION NUMBER: PCT/<br>FILING DATE: 2001-01-30                    |          |
|     | 565                                                           | DATE:                                                                  | ·. ·.    |
|     | 669                                                           | APPLICATIO                                                             |          |
|     | 564                                                           | PRIOR APPLICATION NUMBER: PCT/US01/00664 PRIOR FILING DATE: 2001-01-30 |          |
|     | 667                                                           | PPLICATIO                                                              |          |
|     | ,830                                                          | CURRENT APPLICATION NUMBER: US/10/060,                                 |          |
|     | CONTAINING PROTEIN                                            | E OF INVENTION: HUMAN LCCL DOMAN BETTERSTREE BEALEO                    |          |
|     |                                                               | APPLICANT: Gu, Yizho                                                   |          |
|     |                                                               | Sequence 1114, Application 05/1000030 Publication No. US20030032154A1  |          |
|     |                                                               | 830-1114                                                               | Uπ       |
|     | 0                                                             | ₹.                                                                     | ٥        |
|     | 3                                                             | Y 463 SFLDSRDPASQSQMTSGGDDG 483                                        | γΩ       |
| ٠   | MDMSGHPTTSVGQPSTSTFKATGNQPPPLVGTYNTLLSRTDSCSSAQAQYDTPKAGK 693 | Db 637MDMSGHPTTSVGQPSTSTFKATGNQPPE                                     | b        |
|     | ATGATOVESYORPASPKPVGGGYDKP-AAS 462                            | Qy 405 HTFSTQSGYRVPG-PRPTHKHSHSSGGFPPATGATQVES                         | Ø        |
|     | -GKEAGYADLDPYNSPGQEVYHAYAEPLPITGPEYATPII 636                  | Db 593 FKPEEGKEAGYADLDPYNSPGC                                          | U        |

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RESULT 12
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; ORGANISM: Homo sapiens
US-09-874-198-2
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               Sequence 2, Application US/09874238 Patent No. US20020082209A1 GENERAL INFORMATION:
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APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: 1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING TITLE OF INVENTION: USES FOR IT
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/054,218
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CURRENT FILING DATE: 2001-06-04
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                                                                                                                                                                                                                                                                                                                         DYLLFSSATDQYGPYCGSWAVPKELRLNSNEVTVLF---KSGSHISGRGFLLTYASSDHP 144
                                                                                                                                                                                                                                                                                                                                                                                                                    CGHIVTSQDSGTMTSKNYPGTYPNYTVCEKIITVPKGKRLIL---RLGDLNIESKT-CAS
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                                                                                                                                                                                                                           CPYPMAPPNGHVSPVQAKYILKDSFSIFCETGYELLQGHLPLKSFTAVCQKDGSWDRPMP 359
                                                                                                                                                                                                                                                                                                     DFLKIQTDREEHGPFCGK-TLPHRIETKSNTVTITFVTDESGDH---TGWKIHYTSTAQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686
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Jensenius, Jens Chr
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: Aeomica-X-1
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                                                                                                                                      APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                 APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                    APPLICATION NUMBER:
                                                           FILING DATE:
                                                                          APPLICATION NUMBER: PCT/US01/00664
                                                                                                    FILING DATE:
                                                                                                                   APPLICATION NUMBER: PCT/US01/00667
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                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 24263.6
                     FILING DATE:
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Hanzel, David K.
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NUMBER: PCT/US01/00665
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                                      PCT/US01/00669
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Pred. No. 4.3e-06;
9; Mismatches 97;
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Best Local
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EQ ID NO 45371 
LENGTH: 75
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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INFORMATION:
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Similarity 54.8%;
34; Conservative
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Ashkenazi, Avi
Botstein, David
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                                         Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
                                                                                                                                    Gerritsen, Mary E.
                                                                                                                                                                                                                            Desnoyers, Luc
Eaton, Dan L.
Pan, James
Paoni, Nicholas F
                                                                                      Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                                                                                Ferrara, Napoleone
Filvaroff, Ellen
                             Mather, Jennie P.
                                                                                                                         Goddard
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                                                                                                                                                                  , Sherman
, Wei-Qiang
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EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
EXPRESSED IN BRAIL, SIGNAL = 0.96
EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
EXPRESSED IN PLACENTA, SIGNAL = 1.1
EXPRESSED IN PLACENTA, SIGNAL = 0.9
EXPRESSED IN BORD MARROW, SIGNAL = 0.93
EST_HUMAN HIT: A1565996.1, EVALUE 2.00e-40
SWISSPROT HIT: P98063, EVALUE 1.00e-09
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Pred. No. 7.2e-07;
9; Mismatches 18;
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; ORGANISM: Homo sapiens US-09-905-291A-104
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NUMBER OF SEQ ID NO
SEQ ID NO 104
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                                    195 IHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLFTTPGMNITTVAIP
                                                                                                                                                                                                       112 LRLNSNEVTVLFKSGSHISGRGFLLTYASS------D 142
                                                                                                                                                                                                                                                                                       62 IITVPKGKRLILRLGDLNIES-KTCASDYLLFSSATDQY------GPYCGSWAVPKE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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FILING DATE: 1999-09-15
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                                                                           YPAGVTCVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDS
                                                                                                                      HPDLITC----LERGSHYFEEKYSKFCPAG---CR-DIAGDISGNTKDGYRDTSLLCKAA 194
                                                                                                                                                            LVSSGNKMMVQMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRD
                                                                                                                                                                                                                                              KITVPEGKVVVLNFRFIDLESDNLCRYDFV-----DVYNGHANGQRIGRFCGTFR-PGA 114
                                                                                                                                                                                                                                                                                                                                  GANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTG-ESGFIGSEGFPGVYPPNSKCTW
                                                                                                                                                                                                                                                                                                                                                                                                             6.4%;
1 Similarity 23.3%;
99; Conservation
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·NELLIQFLSDL-SLTADGFIGHY--IFRPKKLPTTTEQPVTT-TFP
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Pred. No. 8e-06;
7; Mismatches 152;
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JRRENT FILING DATE: 2001-07-10
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LICANT: Wood, William, I.
LE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
LE OF INVENTION: Acids Encoding the Same
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                                                              FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-18
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/665,350
                                                                                                                             APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15 APPLICATION NUMBER: PCT/US99/21547 FILING DATE: 1999-09-15
                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/146,222 FILING DATE: 1999-07-28 APPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08
                               APPLICATION NUMBER: PCT/US99/28313 FILING DATE: 1999-11-30
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Gao, Wei-Qiang
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Filvaroff, Ellen
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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art, Timothy A.
NUMBER: PCT/US99/28564
: 1999-12-02
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SEQ ID NO 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 415
TYPE: PRT
383 GEDGR 387
                                                                    335
                                  357 TEEVR 361
                                                                                                      309 TISYDN---
                                                                                                                                                                           255
                                                                                                                                                                                                                                          195 IHAGIITDELGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLFTTPGMNITTVAIP
                                                                                                                                                                                                                                                                                                                                               115 LVSSGNKMYQMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRD
                                                                                                                                                                                                         235 PPAPIVSER-----NELLIQFLSDL-SLTADGFIGHY--IFRPKKLPTTTEQPVTT-TFP
                                                                                                                                                                                                                                                                            175 YPAGVTCVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDS
                                                                                                                                                                                                                                                                                                                143
                                                                                                                                                                                                                                                                                                                                                                               112 LRLNSNEVTVLFKSGSHISGRGFLLTYASS---
                                                                                                                                                                                                                                                                                                                                                                                                                62 KITVPEGKVVVLNFRFIDLESDNLCRYDFV-----DVYNGHANGQRIGRFCGTFR-PGA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
mes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 IITVPKGKRLILRLGDLNIES-KTCASDYLLFSSATDQY------GPYCGSWAVPKE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GAGGPSVLALLFAVCAPLRLQ--AEELGDGCGHIVTSQDSGTMTSKNYPGTYPNYTVCEK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US00/00219 FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/30999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US99/30095 FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
                                                                                                                                                                     SVIFIALLLIGM-GIFAICRKRKKK-----GNPYVSADAQKTGCWKQIKYPFARHQSTEF
                                                                                                                                                                                                                                                                                                              HPDLITC----LERGSHYFEEKYSKFCPAG---CR-DIAGDISGNTKDGYRDTSLLCKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTG-ESGFIGSEGFPGVYPPNSKCTW
                                                                    TVSIINIYKEGNLAIQQAGKNMSARLTVVCK----
                                                                                                                                       -----VTTGLKPTVALCQQKCRRTGTLEGN-YCSSDFVLAG---TVITTITRDGSLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.48;
                                                                                                    EKEMTQKLDLITSDMADYQQPLMIGTGTVARKGSTFRPMDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 170.5; DB 9; Pred. No. 8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                    -QCPLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 107;
                                                                    --- RRGLNYIIMGQV 382
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                                                                                                                                                                                                                                                                                                              194
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